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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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639.5	677.5	694	713.5	714.5	716.5	716.5	726.5	1167	1622	1622	1626	1626	Score	
39.3	41.7	42.7	43.9	43.9	44.1	44.1	44.7	71.8	99.8	99.8	100.0	100.0	Match Length DB	Query
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US-10-097-340-189	US-10-188-186-20	US-10-188-186-24	US-10-104-047-2350	US-10-188-186-22	US-09-833-245-1915	US-09-833-245-1914	US-10-844-874-20	US-10-262-511-184	US-09-895-298-120	US-09-895-298-66	US-10-315-664-75	US-09-978-360A-407	ID	
Sequence 189, App	Sequence 20, Appl	Sequence 24, Appl	Sequence 2350, Ap	Sequence 22, Appl	Sequence 1915, Ap	Sequence 1914, Ap	Sequence 20, Appl	Sequence 184, App	Sequence 120, App	Sequence 66, Appl	Sequence 75, Appl	Sequence 407, App	Description	
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-10-176-747-2	-176-492-2	-10-176-488-2	-10-175-7	-10-175-740-2	7	-10-174-588-	-10-174-582-2	-10-174-579-2	-10-174-57	-10-173-700-2	-10-180-557-2	-10-180-552-	-10-176-913-2	-10-176-757-2	-10-176-482-2	-10-175-752-2	-10-175-738-	-10-173-706-	6-915-2	-10-176-914-	-10-176-749-	-10-176-483-	-10-174-581-	-10-175-	-10-176-758-	0-174-590-	US-10-052-586-206	74-	US-10-398-038-11	-10-288-252-	US-10-094-749-2441
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ALIGNMENTS

Remaining Prior Application data removed - see rile wrapper or FALMI.
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APPLICATION NUMBER: US 09/247,155
NTMBER: PCT/TR98/02122
APPLICATION NUMBER: US 09/215,435
APPLICATION NUMBER: US 09/191,997
FILING DATE: -09-04
30 373
APPLICATION NUMBER: US 60/096,116
APPLICATION NUMBER: US 60/081,563
APPLICATION NUMBER: US 60/074,121
ADDITON TOWNERS IN SO OS9 957
PRIOR APPLICATION NUMBER: US 60/066,677 providence
US/09/978.360A
TITLE OF INVENTION: Complementary DNA's Encoding Proteins
Dumas Milne
Sequence 407, Application US/09978360A

SOFTWARE: Patent.pm EQ ID NO 407

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; NAME/KEY: SIGNAL ; LOCATION: -18..-1 US-10-315-664-75
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SEQ ID NO 75
LENGTH: 302
TYPE: PRT
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FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/10/315,664
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/09/599,360
PRIOR TILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
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US-09-978-360A-407
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Best Local Similarity 100.
702; Conservative
  Best Local Similarity
                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, J.B
APPLICANT: Bougueleret, L.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                       NUMBER_OF_SEQ_ID-NOS:__123_
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal
                                                                                                                   ORGANISM: Homo Sapiens FEATURE:
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ORGANISM: Homo Sapiens
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100.0%; Pred. No. 2.
tive 0; Mismatches
Score 1626; DB 14;
Pred. No. 2.4e-160;
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; NAME/KEY: SITE
; LOCATION: (237)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-895-298-66
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Matches
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SEQ ID NO 66
LENGTH: 302
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                                                                                                                                                                                                                                  Query Match
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PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/591,16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 47 Human Secreted Proteins FILE REFERENCE: PZ03591 CURRENT APPLICATION NUMBER: US/09/895,298 CURRENT FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/112,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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121
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301; Conservative
                                                                                    61 SVPDCKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMQQAPTVGFEADVGQRST
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               LRVVSHTSVÞLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYÞGLQ 180
                                                                 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
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LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
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ID NOS: 231
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Pred. No. 6.2e-160;
0; Mismatches 1;
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                                                                                                                                                                                                                                    DB 10;
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LENGTH: 345
; TYPE: PRT
; CRGANISM: Homo sapiens
GRGANISM: Homo sapiens
; FEATURE:
; NAMB/KEY: SITE
; LOCATION: (280)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
US-09-895-298-120
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US-09-895-298-120
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CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR FILING DATE: 1998-12-17
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.7
Best Local Similarity 99.7
Matches 301; Conservative
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PZ035P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 47 Human Secreted Proteins
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344
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                                                                                                                                                                       181 VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
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                                                                                                                                                                                                                                                                                                                                                                                             1 MKAPGRLVLIILGSVVFSAVYILLGCWAGLPLCLATGLDHHFPTGSRPTVPGPLHFSGYS
                           TE 302
                                                                        EKSHPSVPYHYFEKGRLDECOMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                           EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR 300
                                                                                                                                                VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDXYCR
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99.7%;
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; Pred. No. 7.5e
0; Mismatches
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RESULT 5

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APPLICANT: LOCALING B.
APPLICANT: AGE, MICHELE L.
APPLICANT: AGE, MICHELE L.
APPLICANT: Berghs, Constance
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT FILING DATE: 2001-05-28
PRIOR APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,026
PRIOR APPLICATION NUMBER: 60/328,026
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/373,826
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                                                                                                                                                                    US-10-262-511-184
                                                                                                                                                                                                                          Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 184
LENGTH: 218
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Best Local S
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                                                                                                                                                                                   LENGTH: 218
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                  Local Similarity
nes 218; Conserv
                                           85
MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
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Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
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Peyman, John A.
Kekuda, Ramesh
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Pena, Carol E. A.
Shenoy, Suresh G.
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Rastelli, Luca
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Anderson, David
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Malyankar, Uriel M.
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Spytek, Kimberly A.
Edinger, Shlomit R.
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                                                                               71.8%; Score 1167; DB 15; llarity 100.0%; Pred. No. 9.2e-113; Conservative 0; Mismatches 0;
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US-10-844-874-20
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                                                                                                                     Sequence 1914, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
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Best Local Similarity
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moskal, Joseph
APPLICANT: Yamamoto, Hirotaka
TITLE OF INVENTION: Detection and Treatment
FILE REFERENCE: 97-186-E
CURRENT APPLICATION NUMBER: US/10/844,874
CURRENT FILING DATE: 2004-05-13
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TYPE: PRT
ORGANISM: Rat
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                                                                                                                                                                                                                                                                                                                                                                                                              181
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48.7%; Pred. No. 1.10
tive 46; Mismatches
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; LENGTH: 305
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                                                                                                                                                                                                                                ; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1915
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 129; Conserv
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NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1915
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Best Local Similarity
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546FCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
                       115 VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
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                                                                                                                                         55 HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSABCVFRMNQAPTVGFBAD 114
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52.7%; Pred. No. 1.2e-65;
tive 48; Mismatches 65
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Pred. No. 1.2e-65;
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RESULT 9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-186-22
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CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2002-03-01
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
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SOFTWARE: Custom
SEQ ID NO 22
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                      Matches
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PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
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OR FILING DATE: 2002-03-01
OR APPLICATION NUMBER: 60/304016
OR FILING DATE: 2001-07-09
OR APPLICATION NUMBER: 60/304502
OR FILING DATE: 2001-07-11
OR APPLICATION NUMBER: 60/305262
OR FILING DATE: 2001-07-13
OR APPLICATION NUMBER: 60/373881
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Similarity 52.2%; Pred. No. 1.9e-65;
                                          NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
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AHPSW 299
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                                                                       SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
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No. US20040029789A1
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RESULT 11
US-10-188-186-24
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US-10-104-047-2350
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CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2001-07-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR APPLICATION NUMBER: 60/304502
PRIOR APPLICATION NUMBER: 60/304502
PRIOR PILING DATE: 2001-07-01
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US-10-104-047-2350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEX. 2.1
SEQ ID NO 2350
LENGTH: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/10188186 Publication No. US20040029789A1
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 21402-397C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
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TYPE: PRT
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hes 128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYPNAQIYVTTEKRMSYCDGVFKKETGKDRVQSGSYLSTGWFTFLLAMDACYGIHVYGMI 238
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Matches
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Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See NUMBER OF SEQ ID NOS: 368
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
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TYPE: PRT
                                                                                                                                                                                                                                                                                                   OR APPLICATION NUMBER: 60/360814
DR FILING DATE: 2002-03-01
DR APPLICATION NUMBER: 60/303828
DR FILING DATE: 2001-09-07
DR APPLICATION NUMBER: 60/32380
DR FILING DATE: 2001-09-19
DR FILING DATE: 2001-09-19
DR FILING DATE: 2001-09-19
DR APPLICATION NUMBER: 60/361133
                                         OR APPLICATION NUMBER: 60/305262

OR FILLING DATE: 2001-07-13

OR APPLICATION NUMBER: 60/373881

OR FILLING DATE: 2002-04-19

OR APPLICATION NUMBER: 60/305673

OR FILING DATE: 2001-07-16
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mes 128; Conserv
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APPLICATION NUMBER: 60/304016
FILING DATE: 2001-07-09
                                                                                                                                                                                    APPLICATION NUMBER: 60/304502
FILING DATE: 2001-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/303046 FILING DATE: 2001-07-05
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49.6%; Pred. No. 2.7e-63;
tive 48; Mismatches 66
                   See File Wrapper or PALM
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RESULT 13
US-10-097-340-189
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                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/097,34
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/25,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR PILING DATE: 2001/09/26
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APPLICANT:
APPLICANT:
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-10-188-186-20
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For TITLE OF INVENTION: Assessment, Prevention, and Therapy of FILE REFERENCE: WRI-030
                NUMBER OF SEQ ID NOS:
                                      PRIOR FILING DATE:
                                                      PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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mes 121; Conserv
                                                                                            APPLICATION NUMBER: 60/325,102
                                                                                                              APPLICATION NUMBER: 60/311,732 FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 MYPGLQVYTFTERWMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMV 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 SDSYCREKSHPSVPYHYFEKGRLDECOMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 VGQRST1RVVSHTSVPLLLRNYSHYFQKARDT1YMVWGQGRHMDRVLGGRTYRTL1QLTR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 HY-GYINVKTQBPLQLD-CDLCAIVSNSGQMVGQKVGNBIDRSSCIWRMNNAPTKGYBED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYPNAQIYVTTEKRMSYCDGVFKKETGKDSTEHAVLIDQGWFTFILAMDACYGIHVYGMI
                                                                                                                                                                                                                                                                                                                                                                                                        Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sebastian HOERSCH
Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ami SEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rachel E. MEYERS Michael MORRISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steve G.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10097340 o. US20030087250A1
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ilarity 49.4%;
Conservative 4
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for Windows
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                                      2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOVATS
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Pred. No. 1.4e-
49; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  The Identification, Ovarian Cancer
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APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PACENTIN VET. 2.1
SECTION 02441
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-189
                                                                          ; ORGANISM: Homo sapiens
US-10-094-749-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 189
LENGTH: 336
Query Match 39.3%; Score 639.5; DB 14; Length 336; Best Local Similarity 47.9%; Pred. No. 1.4e-57; Matches 125; Conservative 44; Mismatches 89; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2441, Application US/10094749 Publication No. US20030219741A1
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Best Local Similarity 47.9%;
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                                                                                                              LENGTH: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 GRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 TQQREGVPAGERELDGYLGVADHKEL-KMHCRDCALVISSGHLLHSRQGSQIDQTECVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFR 102
                                                                                                                           336
                                                                                                                                                                                                                                                                                                                                                             IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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SUGIYAMA, 10...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELCDRINVYGMVPPDFCRDPNHPSVPYHYYEPFGPDECTMYLSHERGRKGSHHRFITEKR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECOMYLAHEQAPR-SAHRFITEKA
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WAKAMATSU, AI
SATO, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISHII, SHILLING YAMAMOTO, JUN-ICHI ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTSUKA,
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   Gaps
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; TYPE: PRT
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID
US-10-288-252-11
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US-10-288-252-11
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PRIOR APPLICATION NUMBER: PCT US01/30424
PRIOR APPLICATION NUMBER: PCT US01/30424
PRIOR FILING DATE: 2001-09-28
PRIOR PILING DATE: 2000-11-21
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/249,639
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR APPLICATION NUMBER: US 60/246,001
PRIOR FILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/238,481
PRIOR FILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
                                                                                                                                         SOFTWARE: PERL Program SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10288252
Publication No. US20030143686A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
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APPLICANT:
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APPLICANT:
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FILE REFERENCE: PI-0241 USA
CURRENT APPLICATION NUMBER: US/10/288,252
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 40
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-09-29
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                                                                                                                    ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 TOORPGVPAGPRPLDGYLGVADHKPL-KWHCRDCALVTSSGHLLHSROGSQIDQTECVIR
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Henry
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HAFALIA, April J.A.
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LEE, Ernestine
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TRIBOULEY, Catherine M.
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                    No.
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                        US20030143686A1 2778782CD1
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Query Match
Best Local Similarity 47.5%; pred. No. 2.9e-57;
Matches 124; Conservative 45; Mismatches 89; Indels 3; Gaps 3;

Qy

44 TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFR 102

PD

64 TQQRPGVPAGPRPLDGYLGVADHKPL-KMHCRDCALVTSSGHLLHSRQGSGIDQTECVIR 122

Qy

103 MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYPQKARDTLYMVMGQGRHMDRVLG 162

Qy

163 GRIYRTLLQLTRMYPGLQVYIFTERMMAYCDQIFQDETGKNRRQGSFLSTGWFTMILAL 222

Qy

163 GRIYRTLLQLTRMYPGLQVYIFTERMMAYCDQIFQDETGKNRRQGSFLSTGWFTMILAL 222

Qy

183 GQVINNLHLLSQVLPRLKAFMITRHKMLQFDELFGKDRKISNTWLSTGWFTMTIAL 242

Qy

223 ELCERIVVGMVSDSYCREKSHPSVPYHYFEKGRLDGOMYLAHEQAPR-SAHRPITEKA 281

Db

243 ELCDRINVYGMVPDDFCRDPNHPSVPYHYFEKGRLDGOMYLAHEQAPR-SAHRPITEKA 281

QY

282 VFSRWAKKRPIVFAHPSWRTE 302

QY

283 VFSRWAKKRPIVFAHPSWRTE 302

QY

284 VFSRWAKKRPIVFAHPSWRTE 302

QY

285 VFSRWAKKRPIVFAHPSWRTE 302

QY

286 VFSRWAKKRPIVFAHPSWRTE 302

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287 VFSRWAKKRPIVFAHPSWRTE 302

QY

288 VFSRWAKKRPIVFAHPSWRTE 302

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289 VFSRWAKKRPIVFAHPSWRTE 302

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Abo02791	Abo08739	Abu92662	Abu96231	Abr68178	Abu89929	Abu82808	Abu99569	Abr65629	Abr66239	Abu84365	Abu88050	Abu58502	Aau29126	Aab66105	Aay99356	Aam41144	Aam40096	Aam41882	The state of the s
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ALIGNMENTS

RESULT 1 AAB25764 Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia; septic shock; impotence. 29-JUN-2000. WO200037491-A2. AAB25764; 20-DEC-1999; Homo sapiens. Human secreted protein SEQ ID #76. AAB25764 standard; protein; 302 AA (GEST) GENSET 22-DEC-1998; 25-JUN-1999; 28-NOV-2000 (first entry) portate publication date/ issued 99MO-IB002058. papert filing date / internitedi 98US-0113686P. provid of ate date & database atti

Bougueleret L, Dumas J, Duclert A;

WPI; 2000-442637/38. N-PSDB; AAA87726.

procedures. Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping

Claim 9; Fig 12; 306pp; English.

This sequence represents a human secreted protein amino acid sequence. The invention relates to sequences AAA87725-A87774 which encode human secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for

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RESULT 2
AAB28674
ID AAB2
XX AAB2
AC AAB2
XX AAB2
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XX Huma
XX Huma
XX Huma
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                                                                                                                                                                                                                                                                                                           Human; carbohydrate-modifying enzyme; CME; antidiabetic; immunosuppressive; anti-HIV; antiinflammatory; antianaemic; antiasthmatic; antiarteriosclerotic; antithyroid; hepatotropic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopatiantiarthritic; antipsoriatic; uropathic; ophthalmological; dermatological, antiuleer; cytostatic; virucide; antibacterial; fungicide; protozoacide; tranquiliser; vulnerary; diabetes; autoimmune disorder; inflammatory disorder; infection.
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Pred. No. 1.2e-160;
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(first entry)

AAB61614

standard;

protein; 302

Human protein HP03380.

Human; hydrophobic domain; immune deficiency; autoimmune disorder; allergy; tissue growth; regeneration; wound healing; burn; tumour;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 67-68; 75pp; English.
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Matches 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human proteins (AAB61608-AAB61617) and their coding sequences (AAF28679-AAF28698). The proteins of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 105-106; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human proteins with hydrophobic domains, useful for the treatment of immune disorders, tumors, allergic conditions, thrombosis and microbial
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RESULT 4 - AAB75350

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to 49 Secreted proteins and the clencoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1999;
21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 Secreted
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                                                                                                                                 EKSHPSVPYHYFEKGRLDECOMYLAHEOAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
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99US-00469099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1626; DB 4; 100.0%; Pred. No. 1.2e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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ADD47793 standard; protein;

302

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subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. spene the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
Query Match
Best Local S
Matches 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a bit to be a sequence which is differentially regulated in an animal subjected to pain and a bit to be a sequence which is differentially regulated in an animal subjected to pain and a bit to be a sequence which is differentially regulated in an animal subjected to pain and a bit to be a sequence.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 1017pp;
                                                                                 Sequence 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising preparing a medicament for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003016475-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Protein CAC07404, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004
                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         two or more isolated polypeptides, useful treating pain in an animal.
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                 Score 1626;
Pred. No. 1
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                 DB 7;
.2e-160;
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302;

Conservative

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Mismatches

0

Indels

0

Gaps

proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polypucleotides are useful for express the entire secreted proteins which they encode and for distinguishing human tissues and cells from non-human tissues and cells, and for distinguishing between human tissues and cells that do or do not express the protein and the secret of th

for expressing

express

The invention relates to human cDNA sequences that encode human secreted

Claim 2;

SEQ ID

NO 407; 113pp; English.

the polynucleotides comprising the cDNAs. The polynucleotides and polyneptides are useful in forensic procedures or diagnostic proc

or diagnostic procedures resulting from abnormal

60 0

MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS

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ARBSULT 6
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21-JUN-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                               New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.
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DB; ADP18746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
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Best Local Sim:
Matches 302;
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                                                                                                                                                                                                                                             antiinflammatory; ophthalmological; antirheumatic; antiarthritic; antiangiogenic; cardiant; anti-HIV; nootropic; neuroprotective; antimicrobial; antiparkinsonian; cancer; immune system disorder; angiogenesis; hyperproliferative disorder; cardiovascular disorder; apoptosis; neurological disease; infectious disease; wound healing; chromosome 9.
                                                                                                                                                                                                                                                                                                                                                        Human secreted protein sequence encoded by gene 5 SEQ ID NO:66.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB24441 standard; protein;
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                                                                                                                                                                                                                                                                                                                             Human; secreted protein; cytostatic; antianaemic; antidiabetic;
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 WPI; 2000-431566/37
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                            Rosen CA, Endress GA, Soppet
Shi Y, Lafleur DW, Olsen HS,
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Pred. No. 1.2e-160;
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Forty seven human nucleic acids encoding secreted proteins, treatment, prevention and diagnosis of cancers, disorders of system, angiogenesis disorders, neurological diseases and
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hyperproliferative disorders.
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Claim 11; Page 482-483; 562pp; English.

human secreted proteins given in AAB24437 to AAB24604. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; antianaemic; antidiabetic; antiinflammatory; ophthalmological; antirheumatic; cantidiabetic; antipsoriatic; antiangiogenic; cardiant; anti-HIV; concotropic; neuroprotective; antimicrobial and antiparkinsonian. Human secreted protein polymucleotides, polypeptides, antagonists and/or agonists may be useful in treating, preventing, and/or diagnosing other disorders and/or conditions such as: (a) cancers; (b) calsorders of the immune system; (c) anglogenesis disorders; (d) diseases of the immune system; (e) cardiovascular disorders; (f) diseases hyperproliferative disorders; (e) cardiovascular disorders; (f) diseases appotosis; (g) neurological diseases; and (h) infectious diseases. They are also used to promote wound healing.

AAA78372 to AAA78380 and AAB24436 represent sequences used in the exemplification of the present invention The polynucleotide sequence given in AAA78381 to AAA78432 encode the

Sequence 303 AA;

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                                                                 EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
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AAB24495 standard; protein; 345

Human secreted protein sequence encoded by gene ர SEQ ID NO:120

ARBSULT 8
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XX Hu neuroprotective; antimicrobial; antiparkinsonian; cancer; immune system disorder; angiogenesis; hyperproliferative antiinflammatory; ophthalmological; antirheumatic; antipsoriatic; antiangiogenic; cardiant; anti-HIV; cardiovascular disorder; apoptosis; secreted protein; cytostatic; antianaemic; antidiabetic; cancer; nootropic; antiarthritic; disorder;

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Matches 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infectious diseases. They are also used to promote wound healing. AAA78372 to AAA78380 and AAB24436 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forty seven human nucleic acids encoding secreted proteins, useful in the treatment, prevention and diagnosis of cancers, disorders of the immune system, angiogenesis disorders, neurological diseases and hyperproliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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18-DEC-1998;
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Ji W, Mi Shimkets

3 RA, RULL J. Gangolli

2003-381626/36. DB; ADA05823.

thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; turajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; T, Gorman L, Zerhusen BD, Anderson DM, Zhong M, Catterton W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; mkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipipen AJ, Gangolli EA, Rieger DK, Spaderna SK;

Dipippo

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Patturajan

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing

obesity,

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ADAOS 824
IDAOS 
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16-MAY-2002;
16-MAY-2002;
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17-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator; cytostatic;
                                                                                                                                                                                                                                                                                                                         (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOV44a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           generative disorder; Alzheimer's disease; Parkinson's disease; disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                         CURAGEN
                                                                                                                                                                                                                                                                                                                                                               2002US-0373260P.
2002US-0373815P.
2002US-0373815P.
2002US-0373826P.
2002US-0373824P.
2002US-0374977P.
2002US-0381037P.
2002US-0381038P.
2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
2002US-038335P.
2002US-0393355P.
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2001US-0328029P

2001US-0328044P

2001US-0328849P

2001US-0330142P

2001US-0330142P

2001US-0330142P

2001US-0341058P

2001US-0341058P

2001US-034529P

2001US-034529P

2001US-034529P
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                                                                                                                                                                                                                                                                                                                           CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; nootropic; neuroprotecti
antilipaemic; gene therapy; human c
r; diabetes; obesity; infection; cac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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disorder;

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RESULT 10
ADN62987
ID ADN62
XX
AC ADN62
XY
DT 01-JU
XX
KW humar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC (e.g. NOVI). Also described: (1) a composition comprising a polypeptide CC (e.g. NOVI). Also described: (1) a composition comprising a polypeptide CC containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector CC comprising the babove vector; (6) an antibody that immunospecifically CC comprising the above vector; (6) an antibody that immunospecifically CC comprising the above vector; (6) an antibody that immunospecifically CC comprising the polypeptide described above; (7) methods for determining the CC presence or amount of the above polypeptide or nucleic acid molecule in a cC sample; (8) methods for determining the presence of or predisposition to CC a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a CC method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for CC above; (10) a method for identifying a potential therapeutic agent for CC a pathology associated with the polypeptide; (12) a method for condulating CC a pathology associated with the polypeptide; (12) a method for modulating CC a pathology associated with the above polypeptide in a CC mammal; and (14) a method for producing the above polypeptide in a CC immunomodulator, cytostatic, noctropic, neuroprotective, antiparkinsonian CC acid molecule may be used to diagnose, treat or prevent metabolic CC acid molecule may be used to diagnose, treat or prevent metabolic CC disorders such as diabetes or obesity, infections, cachexia, cancer, CC disorders such as diabetes or obesity, infections, cachexia, cancer, CC disorders and adiabetes or obesity, infections, cachexia, cancer, CC disorders and diabetes or obesity, infections, cachexia, cancer, CC disorders and collectic acids can also be used as hybridisation CC or pathology and collectic acids can also be used as hybridisation the collectic acids ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomics.
present invention.
human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
                                      Human NOV44a
                                                                             01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                           ADN62987 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                 265
                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218;
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                                                                                                                                                                                                                                                                                                                                                                                                                     13
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                                                                                                                                                                                                                                                                                      AHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWRTE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIGSGIGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
                                                                                                                                                                                                                                                                                                                                                                            ROSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECOMYL
                                                                                                                                                                                                                                                                                                                                                                                                                   DTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
                                                                                                                                                                                                                                                            AHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                             (first
                                                                                                                                                                                                                                                                                                                                     TGWFTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECOMYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                       protein;
                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a human
                                                                                                                                                           218
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22-APR-2002;
16-MAY-2002;
16-MAY-2002;
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19-APR-2002;
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19-APR-2002;
                                                                                                                                                                                                                                                                                                                 01-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anorexia; cancer; cancer-associated cachexia; neurodegenerative Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; wasting disorder.
                                                                                                                                                                                                 (SMIT/)
                                                                                                                                                                                                                                            16-MAY-2002;
17-MAY-2002;
                                                                                                                                                                                                                                                                                            19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004038223-A1
                    (ANDE/)
(ZHON/)
(JIWW/)
(MILL/)
(RAST/)
(STON/)
(STON/)
(SHEN/)
(SHEN/)
(SHIM/)
(KOTH/)
                                                                                                              (ORTT/)
                                                                                                                            (LILL/)
(GUOX/)
(PATT/)
(SPYT/)
(EDIN/)
(ELLE/)
                                                                                                                                                                                                                                    28-MAY-2002;
                                                                                                       (ZERH/
                                                                                                                                                                                   (KEKU/)
                                                                                                                                                                                           (PEYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                   /) ELLERMAN K.

) MALYANKAR U M.
) ORT T.
                                 MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R J
AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                              GORMAN L.
ZERHUSEN B 1
ANDERSON D 1
                                                                                                                                                                                   SMITHSON G
MILLET I.
PEYMAN J A
KEKUDA R.
                                                                                                                                                               GGO X
                                                                                                                                                 PATTURAJAN M. SPYTEK K A.
                    LEACH M D.
                            ROTHENBERG
                                                                                   CATTERTON E.
                                                                                           ZHONG
                                                                                                                                                                                                                                                         2001US-0330309P.
2001US-0341058P.
2001US-0343629P.
2001US-0346357P.
2002US-03736357P.
2002US-0373815P.
2002US-0373815P.
2002US-0373815P.
2002US-0373826P.
2002US-037387P.
2002US-0373894P.
2002US-0373894P.
2002US-0381038P.
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2001US-0330142P.
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2002US-0383831P.
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2001US-0328849P.
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2001US-0328044P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CC activity of NOVX polypeptides. For example, NOVX polypeptides and CC polynucleotides may be used to treat disorders associated with decreased CC expression or activity of NOVX by supplementing the pattent our CC production or to rectify mutations. Conversely, antisense NA molecules CC may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX CC polynucleotides and complementary sequences may also be used as DNA CC probes in diagnostic assays to detect and quantitate the presence of CC similar sequences in samples, and so which patients may be in need of CC restorative therapy. NOVX polypeptides may also be used as INA CC probes in diagnostic assays to detect and quantitate the presence of CC (agonists and antagonists) of the expression and activity of NOVX. The cused to modulate NOVX polypeptides may also be used as antigens in CC (agonists and antagonists) of the expression and activity of NOVX. The CC diagnostic agents for detecting the presence of NOVX in samples. NOVX CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX CC diagnose and treat metabolic disorders, diabetes, obesity, infectious cdisease, anorexia, cancer-associated cachexia, neurodegenerative cdisorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, cancer-associated cachexia, metabolic concers. The metabolic syndrome X and cC disturbances associated with obesity, the metabolic syndrome X and cC concersents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated NOVX polypeptides and nucleic acids, diagnosing and treating e.g. cancer, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 184; 395pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patturajan
                                                                                                                                                                                                                                                                                                                                                                   Local
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tturajan M, Spytek KA,
t T, Gorman L, Zerhusen
W, Miller CE, Rastelli
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181
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                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                               al Similarity
217; Conserv
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RIEGER D K.
SPADERNA S K.
AHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWRTE
                        AHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWRTE
                                                                                                              RQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYL
                                                                                                                                                                      DTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNR
                                                                                                                                                                                                 DTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYTFTERMAYCDQIFQDETGKNR
                                                                                                                                                                                                                                                          MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
                                                                                                                                                                                                                                                                                                    MLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKAR
                                                                                   RQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKSEPSVPYHYFEKGRLDECQMYL
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                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Millet I, Peyman JA, Kekuda R, Ju J, Li L,
, Spytek KA, Edinger SR, Ellerman K, Malyanka
an L, Zerhusen BD, Anderson DW, Zhong M, Catt
r CE, Rastelli L, Stone DJ, Pena CEA, Shenoy
Rothenberg ME, Leach MD, Agee ML, Berghs C,
ngolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                               71.3%;
99.5%;
                                                                                                                                                                                                                                                                                                                                           Score 1159; DB 0, Pred. No. 4.2e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for preventing, and Alzheimer's disease.
218
                                                                                                                                                                                                                                                                                                                                                                                     Length 218;
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Malyankar UM;
M, Catterton E;
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                                                                                                                                                                                                                                                                                                       144
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RESULT 11

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14 SVVFSAVYILLCCWAGLPLCLATCLDHHFPT-----GSRPTVPGPLHFS------GY

Matches

Local 146;

Similarity

44.7%; 48.7%;

Score 726.5; DB Pred. No. 9e-67;

DB 7; 85;

Length Indels

23;

Gaps

59

Conservative

46; Mismatches

Sequence

305

Ā,

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ADD47791

XX ADD4

Ratt

XX X ADD4

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                                                                                                     The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent cC that is differentially expressed in neuronal tissue of a first animal cC subjected to pain, a method for identifying an agent cC the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal cC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound that regulates the activity in an animal of one or more of the polynucleotides, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more complication, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more complication and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (Chung), chronic constriction conjured in the sequence data for this patent did not form part of the printed specification, which is differentially expressed during pain. Note:

The sequence data for this patent did not form directly from WIPO at the specification, but was obtained, in electronic form directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENBANK; NP_061996
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01-NOV-2001; 2001US-0346382P.
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                                                                             ftp.wipo.int/pub/published_pct_sequences.
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AAD34106-AAD34144 represent cDNAs corresponding to 17 human secreted protein genes, and AAE21578-AAE21616 represent the proteins they encode. AAE21617-AAE21627 represent human secreted protein fragments. The genes
                                                                                                                                                                                        Seventeen nucleic acid molecules encoding human secreted proteins, useful for treating and preventing cancer, immune disorders (e.g. Addison's disease, and allergies), and cardiovascular disorders (e.g. myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; proliferative disorder; cancer; tumour; AIDS; foetal abnormality; developmental; haematopoietic disorder; kidney; skin; immune system; cardiovascular; angiogenic; gastrointestinal; endocrine; pregnancy-related disorder; cognitive; neurological; autoimmune disease; inflammation; allergy; rheumatoid arthritis; Alzheimer's disease; asthma; Parkinson's disease; schizophrenia; psoriasis; sepsis; atherosclerosis; Parkinson's disease; schizophrenia; psoriasis; sepsis; atherosclerosis; diabetes; infection; wound healing; vulnerary; chemotaxis; food additive;
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                                                                                                           Page 437-438; 483pp; English
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Matches 129
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                                                                                                                                                                                     pregnancy-related disorder; cognitive; neurological; autoimmune disease; inflammation; allergy; rheumatoid arthritis; Alzheimer's disease; asthma
                                                                                                                                                                                                                               Human; secreted protein; proliferative disorder; cancer; tumour; AIDS; foetal abnormality; developmental; haematopoietic disorder; kidney; ski immune system; cardiovascular; angiogenic; gastrointestinal; endocrine;
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                                                                                                                                                                      disease;
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                                                                                                                                                schizophrenia; psoriasis;
wound healing; vulnerary;
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                                                                                                                                                  sepsis; atherosclerosis; chemotaxis; food additiv
                                                                                                                                                                                                                                                                                                                      SEQ ID NO:67.
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                                                                                                                                                                                            disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
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Peptide

1. .30
/label= Signal_peptide Location/Qualifiers Homo sapiens

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AAD34106-AAD34144 represent cDNAs corresponding to 17 human secreted protein genes, and AAE21578-AAE21616 represent the proteins they encode. AAE21617-AAE21627 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing. The therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 17 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of cancer, proliferative disorders, diseases of the immune system, AIDS, autoimmune diseases (rheumatoid arthritis), inflammation, allergies, neurological clisorders (Alzheimer's disease, Parkinson's disease), cognitive disorder, schizophrenia, asthma, skin disorders (psoriasis), sepsis, diabetes, kidney altergraps and control of the cancer of the cancer of the cancer, and cancer of the cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. The present sequence represents a human secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seventeen nucleic acid molecules encoding human secreted proteins, useful for treating and preventing cancer, immune disorders (e.g. Addison's disease, and allergies), and cardiovascular disorders (e.g. myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen
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                                                       SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                                                                                                        IYPNAQIYVTTEKRMSYCDGVFKKETGKDRVQSGSYLSTGWFTFILAMDACYGIHVYGMI
                                                                                                                                                                                                               MYPGIQVYTPTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMV
                                                                                                                                                                                                                                                                                                                                                                                VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEED
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NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
                                                                                                                                                                                                                                                                                                                         VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
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Moore PA, Wei I
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ilarity 52.7%;
Conservative (
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, Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 716.5; DB
Pred. No. 1e-65;
8; Mismatches
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HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEED HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD 129;

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RESULT 14
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XX Albur
KW Albur
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                                                                                                                                                                                  The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The protein X are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. acquired haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldr-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein.  \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
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neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer;
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Score 716.5; DB
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RESULT 15
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS) endocrine disorders (e.g. diabetes), haematopoletic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; human serum albumin; HSA; cancer; reproductive disorder; hispatic disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antilicer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein for treating disease e.g. albumin fused to a therapeutic protein.
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1797-1798; 2102pp; English.
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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Hum. Mol. Genet. 8:1313-1320(1999).

"I-FUNCTION: Involved in the Diosynthesis of ganglioside GDIA from GM1B. Transfers CMP-NeuAc with an alpha-2,6-linkage to GalNAc residue on NeuAc-alpha-2,3-Gall-beta-1,3-GalNAc of glycoproteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF (213-302) FROM N.A. MEDLINE=99299247; FubMed=10369878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
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                                                                                                                                                                                                               between
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                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                    galactosaminyl-R.
PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: T
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TISSUE SPECIFICITY: Ubiquitous.
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RESULT 2
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EMBL; AF127142; AAF00102 1; -.
EMBL; AB035172; BAA87034 1; -.
EMBL; AK003600; BAA91281 1; -.
EMBL; AK000600; BAA9128705 1; -.
EMBL; Y17460; CAB44353 1; -.
EMBL; Y17461; CAB44354 1; -.
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CONFLICT
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                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001675; Glyco_trans_29.
Pfam; PF00777; Glyco_transF_29; T.
Glycoprotein; Glycosyltransferase; Golgi stack; Signal-anchor;
                         Oriol R.;
Submitted (APR-2004) to the
                                                                                                                                                                                                                         Name=siat7D;
                                                                                                                                                                                                                                              Alpha-2,6-sialyltransferase
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                                                                    Harduin-Lepers A.,
                                                                                           SEQUENCE
                                                                                                                                    NCBI_TaxID=9598;
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    AJ646870; CAG26699.1;
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                                                                                       FROM N.A.
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Lumenal, catalytic (Potential).

By similarity.

N-linked (GlCNAc. . .) (Potential).

S -> T (in Ref. 1).

ST -> QA (in Ref. 2).

F -> L (in Ref. 4).

M; 08A4CDC749A6D783 CRC64;
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Last annotation updat
ST6GalNAc IV (Fragmen
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Signal-anchor for type
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SEQUENCE 302 AA; 34
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ
EMBL; AJ646870; CAG26699.1; -.`
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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23-APR-2004 (TrEMBLrel. 27, Last sequence update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-2,6-sialyltransferase ST6GalNAc IV (Fragment)
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  SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDGAECVFRMNQAPTVGFEADVGQRST
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34138 MW; AB7C984AEE53B553
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Pred. No. 5.5e-137;
2; Mismatches 4;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                  AB7C984AEE53B553 CRC64;
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Best Local S
Matches 272
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC
Name-siat7b; Synonyms-ST6GALNAC-IV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
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Pred. No. 3.1e
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RESULT 5
CAF05851
ID CAF05851;
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DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC
Name=siat7b; Synonyms=st6GalNAc-IV;
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                                                                                      SEQUENCE FROM N.A.
Harduin-Lepers A., Martinez-Duncker
                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                              Submitted (JAN-2004)
                                                                        Oriol R.;
                                                                                                                                                                                   Bovinae; Bos
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CAF05850.1; -. F: (alpha-N-acetylneuraminyl-2,3-beta-galactos.
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Cetartiodactyla; Ruminantia; Pecora;
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Pred. No. 3.1e-126;
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cora; Bovidae;
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Best Local Sim
Matches 275;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC
SIAT7B OR STGGALMAC-IV.
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                                                                                                                                                                                                                                                                                                                                                                      "Phylogeny of sialyltransferases.";
Submitted (JAN-2004) to the EMBL/Ge
EMBL; AJ620651; CAP05850.1; -
Glycosyltransferase; Transferase.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
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Oriol R.;
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Pred. No. 6.3e
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Name=Slat7d;
Mus musculus (Mouse).
Nicroota; Metazoa; Chordata;
Netazoa; Rodentia;
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01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Mus musculus 10 days lactation, adult female mammary gl
full-length enriched library, clone:D730030408
product:sialyltransferase 7 ((alpha-N-acetylneuraminyl
betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6
sialyltransferase) D, full insert sequence.
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Q8C3J2;
                    STRAIN-C57BL/6J; TISSUE-Mammary gland;

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Harada A.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
                                                                                                                                                                                                                                                                                      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected
prepare full-length cDNA libraries for rapid discovery
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=20499374; PubMed=11042159;
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STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Mammary gland.
MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Mammary
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium
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Arakawa T., Bono H., Carninci P.,
Arakawa S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Araka Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Araka Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Araka Kurihara C., Matsuyama T., Miyazaki A., Konno H., Kouda M., Koya S.,
Araka Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Araka Mishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Araka K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Araka J., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
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Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
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Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Aragawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
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V. Tagami P
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10090;
[1]

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus musculus (Mouse)

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RESULT 10
AAH56451
ID AAH56
AC AAH56
DT 02-MA
DT 03-MA
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RC STRAIN=C57BL/6; TISUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=2388257; PubMed=12477932;

RX MILSHOPE R.D., Collins F.S., Wangur I.C., Bhat N.K.,

RX Alleschul S.F., Jordan H., Moore T., Max S.I., Mangur I., Hong L.,

RX Alleschul S.F., Jordan H., Moore T., Max S.I., Wangur I., Scheetz T.E.,

RX Alleschul R.F., Johnsholm G.M., Casavant T.L., Scheetz T.E.,

RX Carninci P., Prange C.,

RX Alleschul S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RX Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RX Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RX Raha S.S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RX Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Mahkenjey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX Araywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Araywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Araywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 269
                                 AAH56451 PRELIMINARY;
AAH56451;
02-MAR-2004 (TrEMBLrel. 27, C
02-MAR-2004 (TrEMBLrel. 27, L
02-MAR-2004 (TrEMBLrel. 27, L
51at7d protein (Fragment).
SIAT7D.
          Mus musculus
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Proc. Natl. Acad. Sci. U.S.A.
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Pro; IPR001675; Glyco_trans
PF00777; Glyco_transf_29;
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57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYTFTERMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
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89.1%;
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Last sequence update)
Last annotation updat
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Pred. No. 9.5e-124;
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RESULT 11
SI7D MOUSE
ID SI7D M
AC Q9R2B6
DT 28-FEB
DT 28-FEB
DT 05-JUL
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Garcia A.M., Ganchez A.,
RA Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
RA Rodriguez S., C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences ";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Best Local (
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYFGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKAPGRILLLITLCILTESAVCVFLCCWACLPLCLATCLDRHLPAAPRSTVPGPLHFSGYS
                                                                                                                                                                                                                                                                                                                                                                VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVPDGKPLIRELCHSCAVVSSSGQMLGSGLGAQIDGAECVLRMNQAPTVGFEEDVGQRST
                                                                                                                                                                                                                                                                                   EKSPRSVPYHYFEKGRLDECOMYRLHEOAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                            LRVISHTSVPLLLRNYSHYFQHARDTLYVVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 AA; 35740 MW; 61B8713C0234360D CRC64;
                                                                                                                                                                                                                                            302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1452; DB 2;
Pred. No. 9.5e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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SI7D MOUSE STANDARD; PRT; 360 AA.

9972B6; O887725; Q9JHR0; G95QDP9; Q972B5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3-N-acetyl-

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EMBL; Y15780; CAB43514.1; -. EMBL; Y15780; CAB43515.1; -. EMBL; Y15779; CAB43507.1; -. EMBL; Y15779; CAB43508.1; -. EMBL; A1007310; CAB07446.1; -. EMBL; Y19057; CAB93948.1; -. MGD; MGI:1341894; Siat7d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takashima S., Kurosawa N., Tachida Y., Inoue M., Tsuji S.;
"Comparative analysis of the genomic structures and promoter
activities of mouse Siaa2, 3Galbl, 3GalNAc GalNAc2, 6-sialyltransferase
genes (ST6GalNAc III and IV): Characterization of their Sp1 binding.",
J. Biochem. 127:399-409(2000).
I-FUNCTION: Involved in the biosynthesis of ganglioside GD1A from
GM1B. Transfers CMP-NeuAc with an alpha-2,6-linkage to GalNAc
regidue on NeuAc-alpha-2,3-Gal-beta-1,3-GalNAc of glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Intute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee Y.-C., Kaufman M., Kitazume-Kawaguchi S., Kono M., Takashima S., Kurosawa N., Liu H., Pircher H., Tsuji S., "Molecular cloning and functional expression of two members of mouse NeuAc-alpha-2,3Gal-beta-1,3GalNAc GalNAc-alpha2,6-sialyltransferase family, ST6GalNAc III and IV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  galactosaminide alpha-2,6-sialyltransferase (EC 2.4.99.7) alpha-2,3-Gal-beta-1,3-GalNAC-alpha-2,6-sialvltransferase (IC 2.4.99.7) [Sialyltransferase]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ICR; TISSUE=Brain; MEDLINE=99223522; PubMed=10207017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., ACTIVITY, TISS SPLICING, AND DEVELOPMENTAL STAGE.
                               InterPro; IPR001675; Glyco_trans_29;
Pfam; PF00777; Glyco_transf_29; 1.
                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20198252; PubMed=10731711;
Takashima S., Kurosawa N., Tachida Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 299-360 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q9R2B6-3; Sequence=VSP_001787; TISSUE SPECIFICITY: High expression in lesser extent in lung, heart, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: High expression in brain and colon an lesser extent in lung, heart, kidney, spleen and thymus. DEVELOPMENTAL STAGE: Developmentally regulated. SIMILARITY: Belongs to the glycosyltransferase family 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Glycosylation.
SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuraminyl-(2->3)-beta-D-galactosyl-(1-3)-N-acetyl-D-
galactosaminyl-R = CMP + N-acetyl-alpha-neuraminyl-(2->3)-beta-D-
galactosyl-(1->3)-[N-acetyl-alpha-neuraminyl-(2->6)]-N-acetyl-D-
galactossminyl-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and glycolipids. Prefers glycoproteins to glycolipids. CATALYTIC ACTIVITY: CMP-N-acetylneuraminate + N-acetyl-alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9R2B6-1; Sequence=Displayed;
Name=2; Synonyms=Long 1;
IsoId=Q9R2B6-2; Sequence=VSP_001788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
Event=Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comment=Experimental confirmation may be lacking for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synonyms=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synonyms=Long
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Rodentia;
Glycoprotein; Glycosyltransferase; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       splicing; Named isoforms=3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFICITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kono M., Takashima S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Golgi (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NeuAc-
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RESULT 12
Q6ZXZ0
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Matches
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                      Q6ZXZO;
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
CARBOHYD
                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alpha-2,6-sialyltransferase ST6GalNAc IV (Fragmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal-anchor;
DOMAIN
                                                                                EMBL; AJ646871; CAG26700.1; -. GO:0016757; F:transferase activity, GO; GO:001675; F:transferase 29. InterPro, 1 pro01675; Glyco transf_29; I. pfam; pr00777; Glyco_transf_29; I.
                                                                                                                                                                    STRAIN-Wistar;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Q6ZXZ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                      Glycosyltransferase;
                                                                                                                                Submitted (APR-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                             0210
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                                                                                                                                                      Harduin-Lepers A., Martinez-Duncker I.,
                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                            ΤE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVPDGKPLIRELCHSCAVVSNSGQMLGSGLGAQIDGAECVLRMNQAPTVGFEEDVGQRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                                                                                                                                                                  EKSPRSVPYHYFEKGRLDECQMYRLHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMIPALEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRVISHTSVPLLLRNYSHYFQHARDTLYVVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKAPGRILLITICILTESAVCVFLCCWACLPLCLATCLDRHLPAAPRSTVPGPLHFSGYS
                                 302
302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             302
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134
193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                    ΑA;
                                    302
34332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
283
193
58
                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                             Chordata;
 88.3%;
88.1%;
                                                                      Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.5%;
88.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (Potential).
Lumenal, catalytic (Potential).
By similarity.
N-linked (GlcNac...) (Potential
Missing (in isoform 3).
/FTId=VSP 001787.
MEHVVTCWRLKLLSWPVFLIWICLSLAS -> MEHVVTCWRLKLLSWPVFLIWICLSLAS -> MEHVVTCWRLKLLSWPVFLIWICLSLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1439; Di
Pred. No. 1.7e
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
Score 1436;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
Signal-anchor for type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQRTPIRSF (in isoform 2).
/FTId=VSP 001788.
7CF4101B8FDA369A CRC64;
                                     FA3F65E9B0C25886 CRC64;
                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                            302 AA
                                                                                                        transferring glycosyl.
                                                                                                                                                       Mollicone R.,
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 DB 2;
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23-APR-2004 (TrEMBLrel. 27, Created)
23-APR-2004 (TrEMBLrel. 27, Last sequence update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
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SEQUENCE
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2004) to the EMBL/GenBank/DDBJ EMBL; AJ646871; CAG26700.1; -.
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                                                 VYTFTERMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                                                                                                                                                                                    SVPDGKPLTRELCHSCAVVSSSGQMLGSGLGAQIDGAECVLRMNQAPTVGFEEDVGQRST
                                                                                                                                                                                                                                  SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                                MKARGRILLLILGSITISALYVFICCWACLPLCLATCLDPHLPAPPRSTVPGPLHFRGYS
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88.1%; Pred. No. 2.6e-122;
tive 11; Mismatches 25;
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05-JUL-2004 (TREMBLrel. 27, Last sequence update)
05-JUL-2004 (TREMBLrel. 27, Last sanotation update)
05-JUL-2004 (TREMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC 2.4.99.7).
Name=siat7b; Synonyms=ST6GALNAC-IV;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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EMBL; AJ620653; CAF05852.1; -.

GO; GO:0047290; F: (alpha-N-acetylneuraminyl-2,3-beta-galactos.

GO; GO:0016757; F:transferase activity, transferring glycosyl.

InterPro; IRR001675; Glyco_transf.

Pfam; PF00777; Glyco_transf.29; I.

Glycosyltransferase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RVFVVLLCAAALSVLYVLLCREA-----AGQRD-----GSAYTAPAALSLQGYSRVPDG
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                                                                                                          EEKMAYCDDVFQNETGKNRLKSGSFLSTGWFTMILAMELCEHICVFGMVSDSYCREKNHS
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Pred. No. 6e-87;
3; Mismatches
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CAF05852;
(2-MAR-2004 (TREMBLrel. 27, Created)
02-MAR-2004 (TREMBLrel. 27, Last sequence update)
02-MAR-2004 (TREMBLrel. 27, Last annotation update)
Beta-galactosamide alpha-2,6-sialyltransferase (EC ST6GALNAC-IV OR SIAT7B.

CAF05852

PRELIMINARY;

PRT;

289

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Gallus gallus (Chicken). Eukaryota; Metazoa; Chor

Aves; Neognathae;

Chordata;

Craniata; Ver ; Galliformes;

Vertebrata;

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Phasianidae; Phasianinae;

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                                                                                                                                                                                                           Query Match
64.4%; Score 1047.5; DB 2; Length 289;
Best Local Similarity 66.3%; Pred. No. 6e-87;
Matches 195; Conservative 33; Mismatches 55; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                        Gallus.
NCBI_TaxID=9031;
[1]
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Harduin-Lepers A., Martinez-Duncker I., Mollicone R., Delannoy P.,
Oriol R.;

"Phylogeny of silyltransferases.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

SEMBL; AJ620653; CAF05852.1;

Glycosyltransferase; Transferase.

SEQUENCE 289 AA; 32780 MW; 9FB64C63BA56AF74 CRC64;
6 RLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYSSVPDG 65
                                                                                                                                                                   DB 2; Length 289;
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Search completed: December 10, 2004, 18:25:12 Job time : 194 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 10, 2004, 18:05:03; Search time 40 Seconds
(without alignments)
726.437 Million cell updates/sec
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Title: US-10-019-114A-7
Perfect score: 1626
Sequence: 1 MKAPGRLVLIILCSVVFSAV......FSRWAKKRPIVFAHPSWRTB 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	σ	.4	ω	2	1	No.	Regult
141.5	143	143	144.5	147	153.5	155.5	157	158	164.5	164.5	168	172	172	178	182.5	188.5	190.5	191	196.5	198.5	٠	٠	٠	•	•	•	ω	w	Score	
8.7	•	٠		9.0		9.6	9.7	•	10.1	10.1	٠	10.6	•	10.9	•	•	٠	11.7	12.1	•	12.3	•	12.7		13.6	14.1	4	14.7	₽.) *
375	332	329	375	398	425	342	359	403	526	356	406	375	374	566	413	359	380	343	359	340	359	380	342	337	524	350	350	350	Length	
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	BB	
A46727	9	A48715	I48686	621	T00720	JC5195	JC4973	A28451	JC7248	A54032	A41734	JN0618	A45074	A49880	S41114	I59403	A56950	9	S52425	I54229	N	JC6321	S55675	S36824	JC8017	A54420	JC5251	B54420		
sialyltransferase	ialylt	1-3/1-	alpha 2,	23G	hypothetical prote	alpha-N-acetylneur	GM3 alpha-2,8-sial	beta-galactoside a	alpha-N-acetylgala	alpha-N-acetylneur	acto	ä	ta 1,3	alpha-N-acetylgala	ta 1,4	2,8-pol	2,8-8	ta 1,3GalNA	polysialyltransfer	beta-galactoside a	alpha-N-acetylneur	NeuAc-GM3	Gal-beta-1,3GalNac	beta-galactoside a		beta-galactoside a		beta-galactoside a	cription	

beta-galactoside alpha-2,3-sialyltransferase (EC 2.4.99.4) - human C;Species: Homo sapiens (man) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C;Accession: JC5251; G01021 C;Accession: JC5251; G01021 C;Kim, Y.J.; Kim, K.S.; Kim, S.H.; Kim, C.H.; Ko, J.H.; Choe, I.S.; Tsuji, S.; Lee, Y.C. Biochem. Biophys. Res. Commun. 228, 324-327, 1996 A;Title: Molecular cloning and expression of human Gal beta 1,3GalNAc alpha 2,3-sialytran A;Reference number: JC5251; MUID:97079181; PMID:8920913 A;Accession: JC5251

;Molecule type: mRNA

Status: nucleic acid sequence not shown

ALIGNMENTS

R; Lee, Y. C.; KOjima, N.; Wada, E.; Kurosawa, N.; Makaoka, T.; Hamamoto, T.; Tsuji, S. J. Biol. Chem. 269, 10028-10033, 1994 A; Title: Cloning and expression of cDNA for a new type of Galbetal, eGalNac alpha2,3-sial) A; Reference numbers of cDNA for a new type of Galbetal, eGalNac alpha2,3-sial) A; Recession: B5440: A; Cross: B5440: A; Cross: RENA A; Cross: I-350 (*LEE*) A; Cross: Teferences: UNIPROT:Q11205; GB:X76988; NID:g475225; PIDN:CAA54293.1; PID:g475226 C; Superfamily: beta-galactoside alpha-2,3-sialyltransferase C; Reywords: glycosyltransferase; transmembrane protein Query Match Best Local Similarity 34.3%; Pred, No. 2.2e-13; Matches 71; Conservative 24; Mismatches 80; Indels 32; Gaps 8; Matches 71; Conservative 24; Mismatches 80; Indels 32; Gaps 8; Oy 59 YSSYPDGKPL-VREPCRSCAVVSSGOMLASGICABIDSAECVFRNNQAPTVGFEADV 115 Db 132 FQIVPGENPYRFRDPQQCRRCAVVGNSGNLASGICABIDSAECVFRNNQAPTVGFEADV 191 Oy 116 GQRSTLRVVSHTSVPLLLRNYSHYEQKARDYLYMVWGQGRHMDRVLGGRTVRTL 169
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J. Biol. Chem. 269, 10028-10033, 1994
A;Title: Cloning and expression of cDNA for a new type of Galbetal, eGalNAc alpha2,3-sial A;Reference number: A54420; MUID:94193584; PMID:8144500
A;Accession: A54420
A;Atatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-350 <LEE>
A;Residues: 1-350 <LEE>
A;Cross-references: UNIPROT:Q11204; GB:X76989; NID:g475203; PIDN:CAA54294.1; PID:g475204
C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
C;Keywords: glycosyltransferase; transmembrane protein
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C;Superfamily: beta-galactoside
C;Keywords: glycosyltransferase
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A;Cross-references: UNIPROT:Q16842;
A;Experimental source: liver
R;Giordanengo, V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X96667; NID:g1235530
C;Comment: This enzyme catalyzes the transfer of sialic acid from CMP-NeuAc to the term
substrate preference for glycolipid than for O-linked oligosaccharides of glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: H00561
A; Accession: G01021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-350 <GIO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                  170 LQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIV 229
                                                                                                                                                                                                                                                      59 YSSVPDGKPL-VREP--CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 YSSVPDGKPL-VREP--CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADV
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                    GORSTLRVVSHTSVPLLLRNYSHYFQ--KARDTLYMV----WGQGRHMDRVLGGRTYRTL
                                                                                                                                                                                                      FQIVPGENPYRFRDPQQCRRCAVVGNSGNLRGSGYGQEVDSHNFIMRMNQAPTVGFEKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYGMVSDSYCREKSHPSVPYHYFEKGR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQRSTLRVVSHTSVPLLLRNYSHYFQ--KARDTLYMV----WGQGRHMDRVLGGRTYRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSRTTHHFMYPESAKNLPANVSFVLVPFKVLDLLWIASALSTGQIRF-----TYAPV
                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                   14.1%; Score 228.5; 34.6%; Pred. No. 1.8
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-DKEKVQIYNPAFFKYIHDRWTEHHGRYPSTGMLVLFFALHVCDEVN
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Pred. No. 1.3e-12;
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nes 75;
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A; Map position: 17C
A; Introns: 310/1; 342/3;
C; Keywords: clication
                                                                                                                                                                     A;Cross-references: UNIPROT:P54751; EMBL:X73523; NID:g402214; C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 216, 377-385, 1993
A;Title: Molecular cloning and expression of Gal-beta-1,3GalNAc-alpha-2,3-sialyltransfere
A;Reference number: S36824; MUID:93387288; PMID:8375377
                                                                                                                                                                                                                                                                                                                                                                                                                     beta-galactoside alpha-2,3-sialyltransferase (EC 2 C;Species: Mus musculus (house mouse) C;Date: 22-Jan-1994 #sequence_revision 13-Mar-1997 C;Accession: $36824
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C;Comment: This enzyme is an oligosaccharide-specific enzyme and a type II transmembrane cid to galactose of the Gal beta1,4 GlcNAc structure through an alpha 2,6-linkage.
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R;Takashima, S.; Tsuji, S.; Tsujimoto,
J. Biochem. 134, 287-296, 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-galactoside alpha-2,6-sialyltransferase (EC 2 C;Species: Mus musculus (house mouse) C;Date: 04-Apr-2004 #sequence_revision 04-Apr-2004
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                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-337 < LBE>
                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: $36824
                                                                                                                                                                                                                                                                                                                                                                                                 R;Lee,
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A; Residues: 1-524 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                         Matches
                                                                                                         Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                              Y.C.; Kurosawa, N.; Hamamoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 VYGMVSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 FRMNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKA---RDTLYMVWGQGRHM 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 GWRPLVPGVPLSQLHPRGLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>4</u>5
                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310/1; 342/3; 376/3; 435/1
oligosaccharide-specific; sialyl motif; sialyltransferase; ST6GalII; transmen
                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
  CRRCAVVGNSGNLKDSSYGPEIDSHDFVLRMNKAPTVGFEADVGSRTTHHLV------
                      CRSCAVVSSSGQMLGSGLGABIDSABCVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGFIGILIMMSMCKEVHVYEYIPSVRQTELCH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STGWFTMILALELCEEIVVYGMVSDSYCREKSHPSVPYH--YFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANLNLWYKKPDYNLFTPYIQHRRKYPTQPFYILHPKFIWQLWDIIQENTREKIQPNPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRV-----LGGRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRFNSAPTRGYEKDVGNKTTVRIINSQ----ILANPSHHFIDSALYKDVILVAWDPAPYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSRPTVPG----PLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECV
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                                                                                       Conservative
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                                                                                                         12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.6%; Score 221.5; DB 2; 28.6%; Pred. No. 1.2e-11; tive 38; Mismatches 83;
                                                                                                         Score 209.5; DB 2; Pred. No. 8.3e-11;
                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 T.; Nakaoka, T.; Tsuji,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 2.4.99.4) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EC 2.4.99.1) II -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469
                                                                                                                                                                                                                         PIDN: CAA51919.1;
                                                                                         29;
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                                                                                       Gaps
    187
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                                                                                                                                                                                                                         PID: 940223
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A PARTY CA

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Gene 187, 131-134, 1997

A;Title: Cloning of the cDNA coding for rat brain CMP-NeuAc:GD3 alpha2-8 sialyltra
A;Reference number: JC6321; MUID:97225806; PMID:9073076
A;Accession: JC6321
A;Molecule type: mRNA
A;Residues: 1-380 <ZEN>
A;Cross-references: UNIPROT:P97877; GB:U55938
A;Experimental source: brain
C;Comment: This enzyme is one of the sialyltransferases and adds one more alpha-2, C;Superfamily: alpha-1-acetylneuraminate alpha-2,8-sialyltransferase
C;Keywords: glycosyltransferase
C;Keywords: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
S55675
Gal-beta-1,3GalNac alpha-2,3-sialyltransferase - chicken
Gal-beta-1,3GalNac alpha-2,3-sialyltransferase - chicken
G;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_
C;Accession: S5677
R;Kurosawa, N.; Hamamoto, T.; Inoue, M.; Tsuji, S.
Biochim. Biophys. Acta 1244, 216-222, 1995
                                                                                                                                                                                                                                                                                          N;Alternate names: GD3-synthase; GM3-synthase
;Species: Rattus norvegicus (Norway rat)
C;Date: 14-May-198 #sequence_revision 29-May-
C;Accession: JC6321
R;Zeng, G; Gao, L; Yu, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Molecular cloning and expression of chick Gal-beta-1,3GalNAc alpha-2,3-sialyltr A;Reference number: S55675; MUID:95284088; PMID:7766661 A;Accession: S55675 A;Restatus: preliminary A;Residues: preliminary A;Residues: 1-342 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                     CMP-NeuAc-GM3 alpha2-8 sialyltransferase (EC 2.4.99.-)
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C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 VPG---PLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---HYWE 299
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                                                                                                                                                                                                                                                                     L.; Yu, R.K.
1, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%; Score 206.5;
28.1%; Pred. No. 1.
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                                                                                , 8-lin)
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A;Molecule type: mRNA
A;Residues: 1-359 <70S>
A;Residues: 1-359 <70S>
A;Residues: 1-359 <70S>
A;Experimental source: lung
C;Comment: This enzyme exhibits activity specific toward sialylated glycoproteins. This c;Superimently: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
C;Keywords: glycoprotein; glycosyltransferase; lung; transmembrane protein
F;8-20/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
(;Date: 19-Oct-1995 #sequence_revision 08-Feb-1996
C;Accession: JC4224
R;Yoshida, Y:, KOjima, N:, Tsuji, S.
J. Biochem. 118, 658-664, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;141-185/Region: sialyl signature L F;280-302/Region: sialyl signature S F;50,74,119,204,219/Binding site: carbohydrate (Asn) (covalent) \#status
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                                                                                                                                                              244
                                                                                                                                                                                                       165
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                                                                                                                                                                                                                                                                                                                               125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWPTMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 SLLPDVSPILNKRYNICAVVGNSGILTGSQCGQEIDKSDFVFRCNFAPTEAFHKDVGKKT
                                                                                                                                                                                                                                                                                                                                                                    59 YSSVPDGKPLVREPCRSCAVVSSSGOMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGFLMYTL
LNVLHNRGALK
                                      EKAVFSRWAKK 289
                                                                               TLATRFCDEIHLYGFW--PFPKDLNGKAVKYHYYD---
                                                                                                                                                            ILKNKLQVRTAYPSLRLIHAVRGYWLTNKVPI-----
                                                                                                                                                                                                     TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM
                                                                                                                                                                                                                                                                                     STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW--
                                                                                                                      ILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFIT
                                                                                                                                                                                                                                                SDFITMNPSVVQRAFGGFRNESDREKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASAICEBIHLYGFWPFGFDPNTRE
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 200.5; DB 2; 27.9%; Pred. No. 5.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 202.5; DB Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DLPYHYYDK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 09-Jul-2004
                                                                                 -DLKYRYFSNASPHRMPLEFKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.4.99.8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of N-glycan alpha 2,8-sia
                                                                                                                                                                                                                                                                                                                                                                                                                 45;
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                                                                                                                                                                 -STGLLMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                         164
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I54229
beta-galactoside alpha-2,3-sialyltransferase
C;Species: Homo sapiens (man)

(E)

2.4.99

RESULT 9

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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_ch
C;Accession: I54229; A54898
R;Chang, M.L.; Eddy, R.L.; Shows, T.B.; Lau, J.T.
Glycobiology 5, 319-325, 1995
A;Title: Three genes that encode human beta-galactoside alpl
A;Reference number: I54229; MUID:95383839; PMID:7655169
A;Accession: I54229; MUID:95383839; PMID:7655169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-340 <RES>
A;Cross-references: UNIPROT:Q11201; GB:L13972; NID:g410225;
B;Kitagawa, H.; Paulson, J.C.
J. Biol. Chem. 269, 17872-17878, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem., 269, 17872-17878, 1994
A;Title: Differential expression of five sialyltransferase genes in human A;Reference number: A54898; MUID:94299495; PMID:8027041
A;Accession: A54898
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-11,'V',13-340 <KIT>
A;Cross-references: GB:L29555; NID:g522196; PIDN:AAA36612.1; PID:g522197
C;Genetics:
                                                                                                                                                                                                                                                                                            polysialyltransferase-1 - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Species: Cricetulus griseus (Chinese hamster) C;Chate: 14-7ul-1995 #sequence_revision 21-7ul-1995 #text_change 09-7ul-2004 C;Accession: S52425 R;Sckhardt, M; Muehlenhoff, M.; Bethe, A.; Koopman, J.; Frosch, M.; Gerardy-Schahn, Nature 373, 715-718, 1995 A;Title: Molecular characterization of eukaryotic polysialyltransferase-1. A;Reference number: S52425; MUID:95157675; PMID:7854457 A;Accession: S52425
밁
                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-359 <ECK>
A;Cross-references: UNIPROT:Q64690; GB:Z46801; NID:g735953; PIDN:CAA86822.1; PID:g73595.
C;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
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A;Map position: 3q21-3q28
C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
C;Keywords: glycosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 55
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                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 YPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 LRNYSHYFQKARDTLYMVWGQGRHMD-----RVLGGRTYRTLL------QLTRM 175
                                 59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 CRSCAVVSSSGOMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
  HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DS---KGNWH-----HYWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSYCREKSHPSVPYHYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPAFIKYVFDNWLQGH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---YPESFRELGDNVSMILVPFKTIDLEWVVSAITTGTISHTYIPVPAKIRVKQDKILIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRRCAVVGNSGNLRESSYGPEIDSHDFVLRMNKAPTAGFEADVGTKTTHHLV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%;
                                                                                              12.1%; Score 196.5; DB 2; 27.5%; Pred. No. 1.2e-09; tive 39; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 198.5; DB 2
Pred. No. 7.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRYPSTGILSVIFSMHVCDEVDLYGFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
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                                                                                                                                               Length 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                   45;
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                                                                                                Gaps
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Gal beta 1,3GalNAc alpha 2,3-sialyltransferase - pig C;Species: Sus scrofa domestic (domestic pig) C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change C;Accession: A45073
R;Gillespie, W.; Kelm, S.; Paulson, J.C.
J. Biol. Chem. 267, 21004-21010, 1992
A;Title: Cloning and expression of the Gal beta 1, 3GalNAc alpha A;Accession: A45073; MUID:93016016; PMID:1383214
A;Accession: A45073;
                                                                                                           8
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A;Note: sequence extracted from NCBI backbone (NCBIN:116168, NCBIP:116169)
C;Superfamily: beta-galactoside alpha-2,3-sialyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
 301
                                                                           243
                                                                                                                 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                           124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT
                                                                                                                                                                                                                                                                   67 PLVRE---PCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
                                                                                                                                                                                                                                                                                                         l Similarity
57; Conserv
                                                                                                               FTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKS
   H-----HYWE
                                       HPSVPYHYFE
                                                                           KKEKILIYHPAFIKYVFDRWLQGHGRYPSTGILSVIFSLHICDEVDLYGFGADS--KGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNVLHNRGALK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLATRFCDEIHLYGFW--PFPKDLNGKAVKYHYYD----DLKYRYFSNASPHRMPLEFKT
                                                                                                                                                                                                                             PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFBADVGSKTTHHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKAVFSRWAKK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECOMYLAHEQAPRSAHRFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYRTLLQLTRMYPGLQV-----YTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTM 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDFITMNPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR
                                                                                                                                                                                                                                                                                                           Conservative
 305
                                                                                                                                                                                                                                                                                                                                     11.7%;
                                                                                                                                                                                                                                                                                                                               30.0%;
                                                                                                                                                                                                                                                                                                           36; Mismatches
                                                                                                                                                                                                                                                                                                       Score 191; DB z; -
Pred. No. 3.6e-09;
Pred. No. 77;
                                                                                                                                                   -MILVPFKTTDLEWVISATTTGTISHTYVPVPA-KIKV
                                                                                                                                                                                                                                                                                                                                               Length 343;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha 2,3-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-Sep-1998
                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                 243
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RESULT 12

R;Yoshida, Y.; Kojima, N.; Kurosawa, N.; Hamamoto, T.; Tsuji, S. J. Biol. Chem. 270, 14628-14633, 1995 A;Title: Molecular cloning of Siaalpha2,3Galbeta1,4GlcNAc alpha2,8-sialyltransferase A;Reference number: A56950; MUID:95301555; PMID:7782326 alpha-2,8-sialytransferase III - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: A56950 A56950

A;Accession: A56950 A;Status: preliminary; not compared with conceptual translation

fron

A; Molecule type: mRNA A; Residues: 1-380 < YOS>

A;Cross-references: UNIPROT:Q64689; GB:X80502; NID:g929684; PIDN:CAA56665.1; C;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase C;Keywords: transmembrane protein PID:g929685

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S41114

Gal beta 1,4 GlcNAc alpha 2,6-sialyltransferase - chicken

G;Species: Gallus gallus (chicken)

G;Species: Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S41114

R;Kurossawa, N.; Kawasaki, M.; Hamamoto, T.; Nakaoka, T.; Lee, Y.C.; Arita, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: GUB:rol
A;Cross-references: GDB:1327254
A;Cross-references: GDB:1327254
C;Superfamily: alpha-N-acetylneuraminate alpha-2,8-sialyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-2,8-polysialyltransferase - human
(;Species: Homo sapiens (man)
(;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
(;Accession: 159403
R;Nakayama, J.; Fukuda, M.N.; Fredette, B.; Ranscht, B.; Fukuda, M.
Proc. Natl. Acad. Sci. U.S.A. 92, 7031-7035, 1995
A;Title: Expression cloning of a human polysialyltransferase that forms the A;Reference number: 159403; MUID:95350205; PMID:7624364
A;Recession: 159403
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-359 <RES>
A;Residues: 1-359 <RES>
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C;Genetics:
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Best Local S
Matches 65
                                                                                                                                                                340 LNVLHNRGALK 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 11.6%; Score 188.5; DB 2; Similarity 27.1%; Pred. No. 6.3e-09;
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Pred. No. 4.5e-09;
18; Mismatches 81;
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A; Residues: 1-413 < KUR>
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                      FNLEKQVWKR
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A;Cross-references: UNIPROT:Q92183; GB:X74946; NID:g453196; PIDN:CAA52902.1; PID:g453197 C;Superfamily: alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A49880

R;Kurosawa, N.; Hamamoto, T.; Lee, Y.C.; Nakaoka, T.; Kojima, N.; Tsuji, S.
J. Biol. Chem. 269, 1402-1409, 1994

A;Title: Molecular cloning and expression of GalNAc alpha2,6-sialyltransferase.

A;Reference number: A49880; MUID:94117458; PMID:8288607

A;Accession: A49880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 219, 375-381, 1994
A;Title: Molecular cloning and expression of chick embryo Gal-beta-1,4GlcNAc-alpha-2,6-83
A;Reference number: S41114; MUID:94139712; PMID:8307003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 SGMLGIVIMMTLCDEVDVY-----EFLPSKRQTDI-CHYYQKFHDHACTMGAYH 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 10.9%; Score 178; DB 2; Similarity 25.2%; Pred. No. 9.3e-08; 63; Conservative 37; Mismatches 80
FITEKAVFSR 285
                                                                                                                                                                                                                                                                                                                                                                                                          LRNYSHY-FQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CISCAVVGNGGILNNSGMGQEIDSHDYVFRVSGAVIKGYEKDVGTKTSFYGFTAYSLVSS 396
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                                                                 LLLLTALHLCDRVSAYGYITE ---
                                                                                                                                  FIMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECOMYLAHEOAPRSAHR 275
                                                                                                                                                                                                      FLNYYGRRPRERFDEDFTMNKYLVAHPDFL---RYLKNRFLKSKNLOKPYWRLYRPTTGA
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                                                                                                                                                                                                                                                                       -YTFTERMMAYCDQIFQDETGKNRRQSGSFL--
                                                             -GHQKYSDHYYDK-EWKRLVFYVNHD-
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Search completed: December 10, 2004, 18:25:57 Job time : 41 secs

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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6. /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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1626
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          GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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     US-09-599-360B-75
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US-09-621-976-3915
US-08-446-875-16
US-08-576-775A-2
US-08-972-498-2
US-08-98-9545-2
US-08-98-9545-2
US-08-98-97-442-3
US-08-166-3678-6
US-08-666-3678-6
US-08-166-3678-5
US-08-166-3678-5
US-09-143-438-5
US-08-446-875-10
US-08-466-3678-8
US-09-143-438-8
US-09-134-601-20
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Sequence 4, Appli
Sequence 20, Appli
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ALIGNMENTS

PACENT NO. 75, PACENT NO. 75, PACENT NO. 75, PACENT NEO APPLICANT: APPLICANT: APPLICANT: TITLE OF IN FILE REFERE CURRENT PIL PRIOR APPLI PRIOR APPLI PRIOR APPLI PRIOR FILIN P	_	_	_	<u>.</u>	_		_			
No. 634833 LINFORMATION: LINFORMATION: CANT: Dumas Milne Edwards, J.B. CANT: Dumas Milne Edwa	8	뫄	γQ	B .	₹	Db .	¥	₽ 5	Query Best Match	US-09-59 Sequent Patent GENERAL APPLII APPLI
th Signal Peptides 2; 0; Gaps 0; PGPLHFSGYS 60	EKSHPSVPYHYFEKGRLDECOMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR	VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR	VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR		LRVVSHTSVPLLLRNYSHYFOKARDTLYMVWGOGRHMDRVLGGRTYRTLLOLTRMYPGLO	SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFEADVGQRST	SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST	MKAPGRLVLIILCSVVFSAVXILLCCWAGLFLCLATCLDHHFPTGSRFTVPGFLHFSGYS	atch 100.0%; Score 1626; DB 4; Length 302; Cal Similarity 100.0%; Pred. No. 3.4e-170; Caps 302; Conservative 0; Mismatches 0; Indels 0; Gaps	s99-360B-75 snace 75, Application US/09599360B nt No. 6548633 RAL INFORMATION: LICANT: Dumas Milne Edwards, J.B. LICANT: Bougueleret, L. LICANT: Bougueleret, L. LICANT: Jobert, S. LE OF INVENTION: Complementary DNA's Encoding Proteins with Signal RENT APPLICATION UNMBER: US/09/599,360B RENT FILING DATE: 2000-06-21 OR APPLICATION NUMBER: 60/11,686 OR FILING DATE: 1998-12-22 OR APPLICATION NUMBER: 60/141,032 OR APPLICATION NUMBER: 60/141,032 OR APPLICATION NUMBER: 09/469,099 OR FILING DATE: 1999-12-21 DR APPLICATION WHERER: 09/469,099 OR FILING DATE: 1999-12-21 DR APPLICATION UNBER: 09/469,099 OR FILI

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CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
US-09-334-601-13
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Matches
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APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
TITLE OF INVENTION: NOVEL STALYLTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09334601
Patent No. 6280989
                                                                                                          NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3915
                                                                                                                                                                                                                                                                                            GENERAL
                                                                                                                                                                                                                                                                                                         Sequence 3915, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 47.9%;
                                                                                                                                                               FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: VCUIP-6
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -18..-1
                                                      TYPE: PRT ORGANISM: Homo sapiens
                                                                                         ENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 ELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPR-SAHRFITEKA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 GRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TOORPGVPAGPRPLDGYLGVADHKPL-KMHCRDCALVTSSGHLLHSROGSQIDQTECVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQVYNNLHLLSQVLPRLKAFMITRHKMLQFDELFKQETGKDRKISNTWLSTGWFTMTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                      VFKNWARTFNIHFFQPDWKPE 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELCDRINVYGMVPPDFCRDPNHPSVPYHYYEPFGPDECTMYLSHERGRKGSHHRFITEKR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFSRWAKKRPIVFAHPSWRTE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 639.5; DB 3;
Pred. No. 1.1e-61;
44; Mismatches 89;
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; OTHER INFORMATION: US-09-621-976-3915
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-446-875-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-446-875-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1. Patent No.
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Best Local Similarity
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NAME/KEY: UNSURE
LOCATION: 56
OTHER INFORMATION: 1
NAME/KEY: UNSURE
                                                                                                                                   APPLICATION NUMBER: US/08/446
FILING DATE: July 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/102,38
FILING DATE: AUGUST 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REFERENCE/DOCKET NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                     TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: UNSURE LOCATION: 59
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08446875
                                                                      340 amino acids
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Livingston, Brian Duane
Gillespie, William
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Pred. No. 1.7e-46;
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US-08-503-133A-2
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Matches
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                                                                                                                                                                                                                                              TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/503,133A
FILING DATE: 17-JULY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/04289
FILING DATE: 22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC
                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: BC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION
NAME: Hanson, No. 57473;
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                       Local Similarity
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                                                                                                                                                                                                             LENGTH:
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 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 CRRCAVVGNSGNLRESSYGPEIDSHDFVLRMNKAPTAGFEADVGTKTTHHLV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 DSYCREKSHPSVPYHYFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 HPAFIKYVFDNWLQGH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 LRNYSHYFQKARDTLYMVWGQGRHMD-----RVLGGRTYRTLL------QLTRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 27.8
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York City
HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YPESFRELGDNVSMILVPFKTIDLEWVVSAITTGTISHTYIPVPAKIRVKQDKILIY 247
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805 Third Avenue
                                                                                                                                                                                                            359 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                   12.1%; Score 196.5; DB 1 ilarity 27.5%; Pred. No. 6.4e-13; Conservative 39; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wordperfect
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                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.5 inch, 360 kb storage
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                                                                                                                                                                                                                                                                               688-9200
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, Jun; Bekhardt, Matthias
Isolated Polysiall Transferases,
Nucleic Acid Molecules Coding Therefor, Methods
                                                                                                                                                                                                                                                                                                                                                  5747326man D.
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Pred. No. 3.6e-13;
2; Mismatches 60;
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                                                                                                      DB 1;
                                                                     98;
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                                                                                                      Length
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-576-775A-2
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Patent No. 5849904
  Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                  REGIZENCE NUMBER: BO
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
08/503,133
                                                                                                                                                                                                                                                                                               FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5849904man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/50
FILING DATE: 17-July-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Pollysiallyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
TITLE OF INVENTION: Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfec
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                                                                                                                                                        LENGTH:
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                                                                                                                                    amino acid
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                                                                                                                                                          359 amino acids
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  Conservative
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IBM PS/2
                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-December-1995
12.1%; Score 196.5; DB 2
27.5%; Pred. No. 6.4e-13;
ative 39; Mismatches 98
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                                    DB 2;
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  Indels
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Gaps
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US-08-972-498-2
                                                                                                              ; MOLECULE TYPE: protein US-08-972-498-2
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GENERAL INFORMATION:
                                      Matches
                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
RAPPLICATION UNMERE: 08/576,775
FILING DATE: 21-December-1995
APPLICATION NUMBER: 08/503,133
FILING DATE: 17-July-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/EP94/04
FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5959078man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gerardy-Schahn, Rita; Pukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: Felfe & Lynch
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                    TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
LECTIF -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                      69;
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838-3884
                                                        12.1%; 27.5%;
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                                      39;
                                    Score 196.5; DB 2;
Pred. No. 6.4e-13;
39; Mismatches 98;
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                                        Indels
                                                                          Length 359;
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Patent No.
                                                                      Matches
                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                              TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6020201man
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT:
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,545
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MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acid
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PRIOR APPLICATION DATA:
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                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York City
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125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
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6020201
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                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
                         YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerardy-Schahn, Rita; Fukuda, Minoru;
Nakayama, Jun; Eckhardt, Matthias
VVENTION: Isolated Polysialyl Transferases,
VVENTION: Nucleic Acid Molecules Coding Therefor,
                                                                                                                                                                                                              359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                      12.1%; Score 196.5; DB 3 (Larity 27.5%; Pred. No. 6.4e-13; Conservative 39; Mismatches 98
                                                                                                                                                                                                                                                                                    (212) 688-9200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 kb storage
                                                                                                         DB 3;
                                                                         98;
                                                                                                         Length 359;
                                                                         Indels
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US-08-446-875-2
                                                                                     Matches
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
PILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atent No. 5858751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatenIIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/446,875
FILING DATE: July 12, 1995
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ADDRESSEE: Poms, Smi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Identification and Synthesis
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                                                                                 y Match 11.7%; Score 191; DB 2; Length 343, Local Similarity 30.0%; Pred. No. 2.4e-12; ndels 57; Conservative 36; Mismatches 77; Indels
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ZIP: 90067
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133 PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 TLATRFCDEIHLYGFW--PFPKDLNGKAVKYHYYD----DLKYRYFSNASPHRMPLEFKT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 ILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, Application US/08446875
5. 5858751
                                     67 PLVRE----PCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMQAPTVGFEADVGQRSTLRV 123
                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                   343 amino acids
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2029 Century Park East, Suite 3800
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Gillespie, William
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Wen, Taron, Brian Duane
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of Sialyltransferases
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                                                                                                                                   Matches
                                                                                                                                                                          Query Match
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CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
APPLICATION O4-AUG-1992
TANC DATE: 04-AUG-1992
                                                                                                                                                                                                                                                                                                     TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION UNMEER: 29,421
REFERENCE/DOCKET NUMBER: 97-0
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/102,385G
FILING DATE: 04-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
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                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                         Local
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124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT 183
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                                                                                                                                   1 Similarity 57; Conserv
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                                                          PILEKRIVSCRRCAVVGNSGNIKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHF
                                                                                             PLVRE---PCRSCAVVSSSGOMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
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                                                                                                                                                                                                                                                                                             343 amino acids
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2029 Century Park East, 38th Floor
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                                                                                                                                     Conservative
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Gillespie, William
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Trian Duane
                                                                                                                                 11.7%; Score 191; DB 2; 1 30.0%; Pred. No. 2.4e-12; ative 36; Mismatches 77;
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US-08-626-994A-3
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                                                                                                                                                                                                                                                                                                                                      Query Match
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Shuich
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 77469/1995
FILING DATE: APRIL 3, 1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: 1.44 dis
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                                                                                                                                                                                                                                                                                                                     Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
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FILING DATE: April 3, 1996
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
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                                 221 ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                     212 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                          169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                                 165 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW------IPAFFFHT
                                                                                                                                                                                    120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT 168
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                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                            60 SSVPDGKFLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMQAPTVGFEADVGQRS 119
                                                                                                                                                                                                                                                                                                                     Similarity
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ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
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1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 amino acids
                                                                                                                                                                                                                                                                                                 Conservative
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(703) 716-1180
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Sia` 2,3Gala 1,4GlcNAc ` 2,8-
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                                                                                                                                                                                                                                                                                             Score 190.5; DB 1;
Pred. No. 2.7e-12;
Pred. No. 2.7e-12;
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RESULT 13
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Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Armold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 716-1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlcNAc ' 2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: HOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 339 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Reston
                                                                                              221
                                                                                                                                                                      169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
                                                                                                                                                                                                                                                                                            105 ŚLLPDVSPIMNKRYNVĆAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTEAFHKDVGRKT 164
                                                          268 ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
                                                                                                                                  212 SATVTRTL----VDFFVEHRGOLKVOLAWPGNIMOHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                                                                                                                              165 NLT----TENPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW------IPAFFFHT
                                                                                                                                                                                                                                                  120 TLRVVSHTSVPLLLRNYSHYFQKARDTL-----YMVWGQGRHMDRVLGGRTYRT
                                                                                                                                                                                                                                                                                                                              60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS
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Y: U.S.A.
                                                                                                ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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716-1180
70: 3:
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                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 190.5; DB 3; 30.0%; Pred. No. 2.7e-12; ative 28; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 339;
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US-08-626-994A-1
Sequence 1, Application US/08626994A
Patent No. 5798244
GENERAL INFORMATION:

APPLICANT: Shuichi TITLE OF INVENTION: TITLE OF INVENTION:

Shuichi TSUJI et al.
VENTION: Sia\ 2,3Gala 1,4G1cNAc \
VENTION: SIALYLTRANSFERASE

NUMBER OF SEQUENCES: 4

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEPAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              Sequence 1, Application US/08957742 Patent No. 6017743
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Best Local S
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 77469/1995
RILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
                                                                                                                                                                         GENERAL INFORMATION:
                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C
STEEET: 1941 Roland Clarke Place
                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Perfect 5.1+ (ASCII) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 1.44 di
                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not
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FILING DATE: April 3, 1996
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                                                                                                                                                                                                                                                                                                                 293
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RY: U.S.A.
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                      Reston
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Virginia
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1941 Roland Clarke Place
                                                                                                               Shuichi TSUJI et al.
VENTION: Sia' 2,3Gala 1,4GlcNAc '
VENTION: SIALYLTRANSFERASE
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                                                                                                                                                                                                                                                                               Sequence 6, Application US/08666367B Patent No. 5854042 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOTTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                              TITLE OF INVENTION:
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FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                  COUNTRY: U.
              COMPUTER: IBM Con
OPERATING SYSTEM:
                                                                                                                          STATE:
                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
 SOFTWARE:
                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
                                                                                                                       D.C
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805 Fifteenth
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                                                                                                                                                                                                             VENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR VENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR VENTION: PRODUCING THE SAME
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                                                                                                      U.S.A.
                           E: Diskette,
IBM Compatibl
Wordperfect 5.1
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                                                                                                                                                          Lind & Ponack
Street, N.W., #700
                                                   3.5 inch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.9%; Score 178; DB 2; Length 355; Best Local Similarity 25.2%; Pred. No. 6.8e-11; Matches 63; Conservative 37; Mismatches 80; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,367B
FILING DATE: August 19, 1996
CLASSLFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTER M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                        186 LONLGHKGFKKI------POGKHI-----RYIHFLEAVRDYEWLKALLLDKDIRKG 230
                                                                                                                                                                                                                                                                                      133 LRNYSHY-FOKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQV------ 181
                                                                                                                                                              231 FLNYYGRRPRERFDEDFTMNKYLVAHPDFL---RYLKNRFLKSKNLQKPYWRLYRPTTGA 287
                                                                                                                                                                                                                                                                                                                                  333 FNLEKQVWKR 342
                                                                               288 LLLLTALHLCDRVSAYGYITE-----GHQKYSDHYYDK-EWKRLVFYVNHD------
                                                                                                                      216 FIMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHR 275
                                       276 FITEKAVFSR 285
                                                                                                                                                                                                                                                                                                                                                          73 CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
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Search completed: December 21, 2004, 22:44:59 Job time : 27 secs

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Result
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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716.5
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1622
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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Sequence 75, Appl
Sequence 66, Appl
Sequence 120, App
Sequence 184, App
Sequence 20, Appl
Sequence 1914, App
Sequence 1915, Ap
Sequence 22, Appl
Sequence 2350, App
Sequence 24, Appl
Sequence 20, Appl
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ALIGNMENTS

RESULT 1 US-09-978-360A-407

Sequence 407, Application US/09978360A Publication No. US20040110939A1

PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR PELICATION NUMBER: US 60/069,957
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1998-02-09
PRIOR PELICATION NUMBER: US 60/081,563
PRIOR APPLICATION NUMBER: US 60/086,116
PRIOR PILING DATE: 1998-08-10 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
DUCLERT, Aymeric
APPLICANT:
DUCLERT, Aymeric
APPLICANT:
APPLICANT:
JOBERT, Severin
APPLICANT:
JOBERT, Severin
APPLICANT:
Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.US4.CIP
FILE REFERENCE: 56.US4.CIP PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR TILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17 FILE REFERENCE: 56.US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15 PRIOR APPLICATION NUMBER: US 09/247,155 PRIOR APPLICATION NUMBER: US 60/099,273 Prior Application data removed SEQ ID NOS: 810 See File Wrapper or PALM

Sequence

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APPLICANT: Jobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal TITLE OF INVENTION: Peptides
FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/10/315,664
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US/09/599,360
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 1999-12-21
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SEQ ID NO 407
LENGTH: 302
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Publication No. US20030203377A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 75
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Bougueleret, L. APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 123
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ORGANISM: Homo Sapiens
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Sequence 66, Application US/09895298

Publication No. US20030078405A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
APPLICANT: ROSen et al.
TITLE OF INVENTION: 47 Human Secreted Proteins
FILE REFERENCE: P7035P1

CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT APPLICATION NUMBER: 09/591,16

PRIOR APPLICATION NUMBER: 09/591,16

PRIOR APPLICATION NUMBER: PCT/US99/29950

PRIOR APPLICATION NUMBER: ECT/US99/29950

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/112,809

PRIOR APPLICATION NUMBER: 60/112,809

PRIOR APPLICATION NUMBER: 60/112,809

PRIOR FILING DATE: 1998-12-17

NUMBER: OF SEQ ID NOS: 231
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                                                                                                                                                                                          Matches
                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                 LENGTH: 302
TYPE: PRT
ORGANISM: Homo f
                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
LOCATION: (237)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                          Local Similarity
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                  121 LRVVSHTSVPLLLERNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ 180
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                                                                                 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSABCVFRMNQAPTVGFEADVGQRST 120
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LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ 180
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Pred. No. 6.2e-160;
0; Mismatches 1;
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; NAME/KEY: SITE
; LOCATION: (280)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR PRILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR FILING DATE: 1998-12-17
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 120
LENGTH: 345
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.8%;
Best Local Similarity 99.7%;
Matches 301; Conservative
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TITLE OF INVENTION: 47 Human Secreted Proteins
FILE REFERENCE: PZ035P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
  344
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                                  TE 302
                                                                                                                                                                                                                             LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
TE 345
                                                                                                                                                   VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDXYCR
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b. US20030078405A1
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Pred. No. 7.5e-160;
0; Mismatches 1;
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Gaps

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APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 60/37,917
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/32,917
PRIOR APPLICATION NUMBER: 60/32,029
PRIOR APPLICATION NUMBER: 60/32,029
PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/32,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/32,029
PRIOR APPLICATION NUMBER: 60/32,029
PRIOR APPLICATION NUMBER: 60/32,036
PRIOR APPLICATION NUMBER: 60/32,056
PRIOR APPLICATION NUMBER: 60/32,056
PRIOR APPLICATION NUMBER: 60/32,056
PRIOR APPLICATION NUMBER: 60/32,056
                                                                                 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-262-511-184
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                                                                                                                                                              Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 184, Application US/10262511 Publication No. US20040038223A1 GENERAL INFORMATION:
  Matches
                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
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                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/327,435
  218;
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Peyman, John A.
Kekuda, Ramesh
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Rastelli, Luca
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Anderson, David W.
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Agee, Michele L.
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  ilarity 100.0%;
Conservative (
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71.8%; Score 1167; DB 15; 100.0%; Pred. No. 9.2e-113; ive 0; Mismatches 0;
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US-10-844-874-20
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US-09-833-245-1914
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; NAME/KEY: misc feature
; OTHER INFORMATION: rat alpha 2, 6-ST
US-10-844-874-20
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CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/10844874 Publication No. US20040204381A1 GENERAL INFORMATION:
                                                                                                                                             Sequence 1914, Application US/09833245 Publication No. US20040010134A1 GENERAL INFORMATION:
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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
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TYPE: PRT
ORGANISM: Rat
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APPLICANT: Yamamoto, Hirotaka
TITLE OF INVENTION: Detection and Treatment of Glyco-Enzyme-Related Disease
FILE REFERENCE: 97-166-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 Match 44.7%; Score 726.5; DB 17; Length Local Similarity 48.7%; Pred. No. 1.1e-66; hes 146; Conservative 46; Mismatches 85; Indels
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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1915
LENGTH: 305
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PRIOR FILING DATE: 2000-12-21
PRIOR PPLICATION NUMBER: 60/199, 3:
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1914
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US-09-833-245-1915
; Sequence 1915, Application US/09833245
; Publication No. US20040010134A1
; Publication No. US20040010134A1
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US-09-833-245-1915
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Best Local Similarity
                                                                                                                                                   Matches
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
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TYPE: PRT
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                                                                                                HFSGYSSVFDGKFLVREFCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAFTVGFEAD 114
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                   VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
                                                                          HY-GYINVKTQEPLQLD-CDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEED
VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG 178
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ilarity 52.7%;
Conservative 4
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52.7%; Pred. No. 1.2e
ative 48; Mismatches
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                                                                                                                                                     Score 716.5; DB :
Pred. No. 1.2e-65;
lB; Mismatches 6!
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US-10-188-186-22
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SEQ ID NO 22
SEQ IDNO 25
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CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILLING DATE: 2001-07-05
PRIOR FILLING DATE: 2002-03-01
PRIOR FILLING DATE: 2002-03-01
PRIOR PRILORITION NUMBER: 60/303828
PRIOR FILLING DATE: 2001-09-07
PRIOR PRILOR DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILLING DATE: 2001-09-19
PRIOR FILLING DATE: 2001-09-19
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Best Local S
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TYPE: PRT
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APPLICATION NUMBER: 60/305262
FILING DATE: 2001-07-13
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FILING DATE: 2001-07-09
APPLICATION NUMBER: 60/304502
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FILING DATE: 2002-03-01
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                   239 NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
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                                                                                               IYPNAQIYVTTEKRMSYCDGVFKKETGKDRVQSGSYLSTGWFTFLLAMDACYGIHVYGMI
                                            SDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVF
                                                                                                                                                                             VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
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                                                                                                                                                                                                                                                                                                                                            43.9%; Score 714.5; DB 1 ilarity 52.2%; Pred. No. 1.9e-65; Conservative 49; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-07-16
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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 2350
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2350
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US-10-188-186-24
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US-10-104-047-2350
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Best Local Similarity
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC
FILE REFERENCE: 21402-397C
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CURRENT FILING DATE: 2002-03-25
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                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/303046
PRIOR FILING DATE: 2001-07-05
                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
                                                                                                                                                        PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/360814
                                                                        FILING DATE: 2001-09-07
APPLICATION NUMBER: 60/323380
FILING DATE: 2001-09-19
APPLICATION NUMBER: 60/361133
                                    APPLICATION NUMBER: 60/304016
                                                         FILING DATE: 2002-03-01
APPLICATION NUMBER: 60/304502
                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 VGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 HFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEAD 114
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                2001-07-09
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52.2%;
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; Pred. No. 2.4e-65;
49; Mismatches 65
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PRIOR APPLICATION NUMBER: 60/305262
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/303673
PRIOR FILING DATE: 2001-07-16
Remaining Prior Application data removed - Set
NUMBER OF SEQ ID NOS: 368
SOFTWARE: Custom
SEQ ID NO 24
LENGTH: 318
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Publication No.
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-10-188-186-24
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CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
Remaining Prior Application data removed - See File Wrapper or PALM.
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                                   FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/323380
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/360814 FILING DATE: 2002-03-01
                                                                                                                            APPLICATION NUMBER: 60/305262
                                                                                                                                                                                                  APPLICATION NUMBER: 60/304016
                                                                                                                                                                                                                  APPLICATION NUMBER: 60/361133 FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/303828
                                                       APPLICATION NUMBER: 60/305673
                                                                                       FILING DATE: 2001-07-13
APPLICATION NUMBER: 60/373881
                                                                                                                                               FILING DATE:
                                                                                                                                                                APPLICATION NUMBER: 60/304502
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                                                                  CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 05/276,025
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-03-17
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-08-26
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
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                                 PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305
                  SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDTYCKTEGYRKVPYHYYEQGR-DECDEYFLHEHAPYGGHRFITEKKVFAKWAKKHRIIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGRMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVG
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Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rachel E. MEYERS Michael MORRISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steve G. KOVATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sebastian HOERSCH
Shubhangi KAMATKAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peter OLANDT
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for Windows Version
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PRIOR APPLICATION NUMBER: 60/350, 435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2441
LENGTH: 336
TYPE: PRT
                                                                       ; ORGANISM: Homo sapiens
US-10-094-749-2441
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Query Match 39.3%;
Best Local Similarity 47.9%;
Matches 125; Conservative 4
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Best Local Similarity 47.9%;
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                                                                                                                                                                                                                                                                    APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENUI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
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blication No. US20030219741A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GRTYRTLLQLTRMYPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILAL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFR 102
                                                                                                                                                                                                                                                                                                                                                                                              OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMBCHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLCDRINVYGMVPPDFCRDPNHPSVPYHYYEPFGPDECTMYLSHERGRKGSHHRFITEKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQVYNNLHLLSQVLPRLKAFMITRHKMLQFDELFKQETGKDRKISNTWLSTGWFTMTIAL
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 44; Mismatches
                Score 639.5; DB 14;
Pred. No. 1.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 639.5; DB 14; Length Pred. No. 1.4e-57;
 Indels
                               Length 336;
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Gaps
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RESULT 15
US-10-288-252-11
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                                                                                                         PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 11
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Publication No. US20030143686A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/288,252
CURRENT FILING DATE: 2002-11-04
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/252,819
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/249,639
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PRIOR FILING DATE: 2001-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: PI-0241 USA
                                                 LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/247,931
               FEATURE: NAME/KEY: misc_feature
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OTHER INFORMATION: Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION: TRANSFERASES
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/246,001 FILING DATE: 2000-11-03
                                                                                                                                                                                                      APPLICATION NUMBER: US 60/238,481 FILING DATE: 2000-10-06
                                                                                                                                                                                                                                         APPLICATION NUMBER: US FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNQAPTVGFEADVGQRSTLRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQQRPGVPAGPRPLDGYLGVADHKPL-KMHCRDCALVTSSGHLLHSRQGSQIDQTECVIR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFSRWAKKRPIVFAHPSWRTE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPR-SAHRFITEKA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANG, Y. TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELCDRINVYGMVPPDFCRDPNHPSVPYHYYEPFGPDECTMYLSHERGRKGSHHRFITEKR 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRIFFIN, Jennifer A.
SANJANWALA, Madhu S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRIFFIN, Jennifer
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TRIBOULEY, Cath
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GANDHI, Ameena R.
WARREN, Bridget A.
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                                                                                                                                                                2000-09-29
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No. US20030143686A1 2778782CD1
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Command line parameters:

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-DB=Issued Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=5bite -STARTS1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NORM-DARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPPEXT=0.5 -FGAPOP=6
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No.
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Maximum
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Listing first 45 summaries
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-334-601-12

US-09-620-312D-401

US-09-621-976-55

US-08-503-133A-1

US-08-576-775A-1

US-08-972-498-1

US-08-98-545-1

US-08-446-875-15

US-08-446-875-15

US-08-446-875-15

US-08-446-875-15

US-08-466-875-15

US-08-626-994A-4
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Sequence 1, App	'n	6,	e 11,	e 11, /	e 46	7,	Sequence 5, Ap	12	'n	4,	Sequence 4, Ap	μ,	9	ω `	ω	e 1,	μ,	e 2,	2	e 9,	e 9,	e 8,	ю 89 ,	equence 8,	е 80 ,	e 7,	e 7,	e 7,	e 7,	equence 2,	equence 2,	Sequence 4, Ap
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ALIGNMENTS

US-09-599-360B-25

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Sequence 25, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Bougueleret, L.
APPLICANT: Bougueleret, L.
APPLICANT: JObert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENERI US/09/599,360B
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 1908-12-22
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 25
LENGTH: 1556
TYPE: DNA
CREANISM: Homo Sapiens
FEATURE:
NAME/KEY: Sig_beptide
LOCATION: 261..1166
NAME/KEY: Sig_beptide
LOCATION: 261..314
OTHER INFORMATION: SCOTE 8.80
OTHER INFORMATION: SCOTE 8.80
OTHER INFORMATION: SECTE 8.80
OTHER INFORMATION: SECTE 8.80
OTHER INFORMATION: SECTE 8.80
LOCATION: 1524..1556
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Best I Query DB:

Percent Similarity:
Best Local Similarity:
Query Match:

3.61e-179 1626.00 100.00% 100.00% 100.00%

Alignment

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US-10-019-114A-7 (1-302)

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TyrIleLeuLeuCysCysTrpAlaGlyLeuProLeuCysLeuAlaThrCysLeuAspHis
                                                                AlaValPheSerArgTrpAlaLysLysArgProIleValPheAlaHisProSerTrpArg
                                                                                                                       GlnMetTyrLeuAlaHisGluGlnAlaProArgSerAlaHisArgPheIleThrGluLys
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APPLICANT: Kapitonov, Dmitri
APPLICANT: Kapitonov, Dmitri
APPLICANT: N., Robert
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 2056
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Patent No. 6280989
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LOCATION: (181)..
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AlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgValLeuGly :::::: ||||:::::: ||||
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                                                           ThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePheGlnAspGluThrGlyLys
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                                                                                                                       ATGATTACTCGCCACAAGATGCTGCAGTTTGATGAGCTCTTCAAGCAGGAGACTGGCAAA
                                                                                                                                                                                   GGCCAGGTCTÁCAACAACCTGCATCTCCTGAGCCAGGTGCTGCCCCGGCTGAAGGCCTTC
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
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                                                                                                              US-10-019-114A-7 (1-302) x US-09-620-312D-401 (1-2697)
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US-09-620-312D-401
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SOFTWARE: pt Ft genes Version 1.0
SEQ ID NO 401
LENGTH: 2697
TYPE: DNA
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NAME/KEY: CDS
LOCATION: (135)..(1136)
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                                                                                                                                                                                                                                              No.:
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                                          323 TGCCAATGAGGTCTTCCATTACGGCTC--
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   46 SerArgProThrValProGlyProLeu--
                                                                CysTrpAlaGlyLeuProLeuCysLeuAlaThrCysLeuAspHisHisPheProThrGly
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Asundi, Vinod
Zhang, Jie
Ren, Feiyan
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Chen, Rui-hong
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Zhou, Ping
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Yang, Yonghong
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Matches:
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 ----HisPhe-SerGlyTyrSerSerVa
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                                          CCTGCGGGG
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                                                                     CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 55
LENGTH: 546
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-621-976-55
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                     Sequence 55, Application US/09621976 Patent No. 6639063
                   FEATURE:
NAME/KEY: CDS
LOCATION: 260.
LOCATION: 260..544
NAME/KEY: sig_peptide
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Best Local Similari
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US-08-503-133A-1
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DB:
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OTHER INFO
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor,
TITLE OF INVENTION: Production and Use
                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
CAPPLICATION UMBER: US/08/503,133A
FILLING DATE: 17-JULY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Disketto
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC
   NAME: Hanson, No. 5747326man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                               APPLICATION NUMBER: PCT/EP94/04289
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      STATE: N
                                                                                                                                                                                                                                                             STREET:
CITY: N
                                                                                                                                                                                                                                                                                       ADDRESSEE:
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R INFORMATION:
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805 Third Avenue
                                                                                                                                                                                                                                        USA
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score 8.80000019073486
seq RLVLIILCSVVFS/AV
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US-10-019-114A-7 (1-302) x US-08-503-133A-1 (1-2026)
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                                                  uAlaHisGluGlnAlaProArgSerAlaHisArgPheIleThrGluLysAlaValPheSe 284
                                                                                                          AAAAGCTGTGAAATATCATTACTACGAT---
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Best Local Similarity:
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US-08-576-775A-1
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GENERAL INFORMATION:
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APPLICATION NUMBER: 08/503,133
FILING DATE: 17-July-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/ED94/042
FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 111
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                          No.:
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MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor,
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LOCATION:
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STATE: New York
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GENERAL INFORMATION:
APPLICANT: Gerardy-Sch
APPLICANT: Nakayama, J
TITLE OF INVENTION: IS
TITLE OF INVENTION: Nu
TITLE OF INVENTION: Pr
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                     COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DO
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York City
STATE: New York
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805 Third Avenue
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Nakayama, Jun; Eckhardt, Matthias
VENTION: Isolated Polysialyl Transferases,
ENTION: Nucleic Acid Molecules Coding The
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/04289
APPLICATION NUMBER: PCT/EP94/04289
FILING DATE: 22-December-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5959078man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1050.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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LOCATION:
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               uCysGluGluIleValValTyrGlyMetValSerAspSerTyrCysArgGluLysSerHi 244
                                                                                              gArgGlnSerGlySerPheLeuSerThrGlyTrpPheThrMetIleLeuAlaLeuGluLe 224
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TIGIGATGAAATTCACCIGIATGGGTTCIGG-----CCCTTCCCTAAGGATTTGAAIGG 1226
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Matches:
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10-019-114A-7 (1-302) x US-08-899-	Alignment Scores: 1.47e-12 Pred. No.: 196.50 Score: 196.50 Percent Similarity: 45.93% Best Local Similarity: 28.86% Query Match: 12.08% DB: 3	HIT 8 8-89-545-1 gquence 1, Application US/08899545 tent No. 6020201 tent No. 6020201 peneral INFORMATION: APPLICANT: Gerardy-Schahn, Rita; APPLICANT: Gerardy-Schahn, Rita; APPLICANT: Nakkayama, Jun; Eckhar; TITLE OF INVENTION: Isolated Pol- TITLE OF INVENTION: Isolated Pol- TITLE OF INVENTION: Production a NUMBER OF SEQUENCES: ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York COUNTRY: USA ZIF: 10022 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inc COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inc COMPUTER: IBM PS/2 OPERATING SYSTEM: PC-DOS SOPTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/899, FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: 08/503,133 APPLICATION NUMBER: 08/503,133 APPLICATION NUMBER: 08/503,133 APPLICATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: BOER TELEPHONE: 2026 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) FEATURE: LOCATION: 3011377 08-899-545-1	284 rArgTrpAlaLysLys 289 135 1335 CAGAGGAGCACTAAAA 1350		244 sproSerValProTyrHisTyrPheGluLysGlyArgLeuAspGluCysGlnMetTyrLe
545-1 (1-2026)	Length: Matches: Conservative: Mismatches: Indels: Gaps:	Fukuda, Minoru; dt, Matthias gsialyl Transferase Molecules Coding T nd Use h, 360 kb storage 1050		::: GAT AlaHisArgPheIle CCATTAGAATTCAAA	GluLysGlyArgLeu
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US-08-446-875-15
; Sequence 15, Application US/08446875
; Patent No. 5858751
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APPLICANT: 1
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                                                                                                                                                                                           APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of
                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                      NUMBER OF SEQUENCES:
  COMPUTER READABLE FORM:
                                                                                   STREET: 2029 Centi
                                          COUNTRY:
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                                                                                                     2029 Century Park East,
                                                                                                                                                                                                                                                                                                Paulson, James C.
Wen, Xiaohong
Livingston, Brian Duane
Gillespie, William
                                          USA
                                                                                                                              Poms, Smith, Lande & Rose
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                                                                                                          Suite 3800
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
PILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (310) 277-12
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: July 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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                                                                                                                                                                                                                                                            700 CCTGCAAAGATCAGAGTGAAACAGGATAAGATCCTGATCTACCACCCCAGCCTTCATCAAG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 LeuArgAsnTyrSerHisTyrPheGlnLysAlaArgAspThrLeuTyrMetValTrpGly 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 GAGATAGACAGTCACGACTTTGTCCTCAGGATGAACAAGGCGCCCACGGCAGGGTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 TGCCGGCGCTGCGCCGTTGTGGGCCAACTCGGGCAACCTGAGGGAGTCTTCTTATGGGCCT 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 CysArgSerCysAlaValValSerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAla
  ATGCATGTCTGCGATGAGGTGGACTTGTACGGCTTCGGGGCAGACAGC-----AAAGGG
                             LeuGluLeuCysGluGluIleValValTyrGlyMetValSerAspSerTyrCysArgGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACATAATGTCAGCATGATCCTGGTGCCCTTCAAG---ACCATCGACTTGGAGTGG---
                                                                                                                            LysAsnArgArgGlnSerGlySerPheLeuSerThrGlyTrpPheThrMetIleLeuAla
                                                                                                                                                                         TATGTCTTTGACAACTGGCTGCAAGGGCAC-
                                                                                                                                                                                                                 TyrThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePheGlnAspGluThrGly 201
                                                                                                                                                                                                                                                                                                                                                                                          GlnGlyArgHisMetAspArgValLeuGlyGlyArgThrTyrArgThrLeuLeu-----
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Matches:
Conservative:
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US-10-019-114A-7 (1-302) x US-08-446-875-1 (1-1218)
                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-446-875-1
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION LONTA:
APPLICATION NUMBER: US/08/446,875
FILING DATE: July 12, 1995
CLASSIFICATION NUMBER: 08/102,385
FRILING DATE: AUGUST 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REGISTRATION NUMBER: 29,421
REGISTRATION NUMBER: 111-197
TELECOMMUNICATION: NTORWATION:
TELEPHONE: (310) 788-5000
TELEPHONE: (310) 788-5000
TELEPAX: (310) 779-1297
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTIF. TYPE: CDNA
                                                                                                                                       Pred. No.:
                                                                                                                                                      Alignment Scores:
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Patent No. 5858751
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NAME/KEY: CDS
LOCATION: 91..1119
OTHER INFORMATION: /
OTHER INFORMATION: C
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: porcine
TISSUE TYPE: liver, submaxillary glands
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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CITY: Los Angeles
STATE: CA
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ZIP: 90067
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2029 Century Park East, Suite 3800
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Wen, Xiaohong
Livingston, Brian Duane
Gillespie, William
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192.50
46.79%
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GalNAc alpha 2,3 sialyltransferase"
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Matches:
Conservative:
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PREPEROTHRIQUE ARAPPRO-THEVIAL PROGRAMCETGO-CLEHIS PRESERCITY TO STATE AND ARAPSE AND AR	08-102-385 08-102-385 equence 1, atent No. GENERAL IN APPLICAN APP	75	36	16	ភ	96	76 98	38	36	16	96	76 25	84	4 0	40
	ation US/08102385G i (N): Ilson, James C. 1, Xiaohong Vingston, Brian Duane llespie, William lm, Sorge lingame, Alma L. Pringame, Alma L. Pringestions and Methods for the Prons: Identification and Synthesis of Sialyltransferase Prons: 36 ADDRESS: ADDRESS: ADDRESS: Pringame, Pringame, Bast, 38th Floor Release #1.0, Version #1.25 ANTION DATA:	AGCCACTACTGGCACCACTACTGGAG 100	rPheGlu 25	v v	9	N	ProGlyLeuGlnValTyrThrPheThrGluArgMetMetAlaTyrCy8AspGlnIlePh 1		HisTyrPheGlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHi 		Ф 1	un vo	ហ	CAGGGAGCIGITICCAGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGI	PheProThrGlySerArgPro-ThrValProGlyProLeuHisPheSerGlyTy

US/08/102,385G

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FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925369
FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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OTHER INFORMATION:
OTHER INFORMATION:
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REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: porcine TISSUE TYPE: liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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798
                                   176 rProGlyLeuGlnValTyrThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePh 196
                                                                                                                  156 sMetAspArgValLeuGlyGlyArgThrTyrArgThrLeuLeuGlnLeuThrArgMetTy
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CCCCGCC---AGATCAAAGTCAAAAGGAGAAGATCCTGATTTATCACCCGGCCTTCAT 854
                                                                           CCTGGAGTGGGTGATCAGCGCCACCACCACCGGCACCATCTCCCCACACCTACGTTCCTGT
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11.84%
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GalNAc alpha 2,3 sialyltransferase"
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
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US-08-626-994A-4
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                                                                                                                                              US-10-019-114A-7 (1-302) x US-08-626-994A-4 (1-1048)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 77/
FILING DATE: APPLI 3, 1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Shuich
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1048 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia'.2,3Gala 1,4G1cNAc'
TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Word Perfect 5.1+ (ASCII)
                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Greenblum & Bernstein, P.L.C. STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  855 CAAGTACGTCTTCGACAGGTGGCTGCAGGGCCACGGGCGCTACCCGTCCACTGGCATCCT 914
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386 GGAAACAGTGGAATCTTGACAGGGAGTCAGTGTGGACAAGAAATAGATAAATCAGATTTT 445
                                                                        326 TCCCTGCTCCCAGATGTGTCGCCCATTATGAATAAGCGTTATAATGTTTGTGCTGGTGGTT
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                             80 SerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCys 99
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44.29%
30.95%
11.72%
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Matches:
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RESULT 13
US-08-957-742-4
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Patent No. 6017743
GENERAL INFORMATION:
                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC'
TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                       ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia COUNTRY: U.S.A.
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; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-08-957-742-4
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Query Match:
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                                                                                                                                      Sequence 2, Application US/08626994A Patent No. 5798244
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SEQUENCE CHARACTERISTICS:
LENGTH: 1048 bases
                                                                                                   GENERAL INFORMATION:
APPLICANT: Shuich
                         APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4G1CNAC
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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           ADDRESSEE:
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                                                                                                                                                                                                                                     ---GATCTGCCCTACCACTACTATGACAAA
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                                                                                                                                                                                                                                                                                                                                             ilevalValTyrGlyMetValSer-----AspSerTyrCysArgGluLysSerHis
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           Greenblum & Bernstein,
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Best Local Similarity:
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APPLICATION NUMBER: JP 7:
FILING DATE: April 3, 19:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 716-1191
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STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
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                                         190 AlaTyrCysAspGlnIlePheGln-----AspGluThrGlyLysAspArgArgGlnSer
                                                                                                                              171 GlnLeuThrArgMetTyrProGly---LeuGlnValTyrThrPheThrGluArgMetMet 189
                                                                                                                                                                            798 ATACTTTGGATCCCTGCATTTTTCTTCCACACTTCTGCAACTGTAACGAGAACGCTAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                120 ThrLeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyr 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 ValPheArgMetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSer 119
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GCTTGGCCTGGAAATATCATGCAACATGTCAACAGGTACTGGAAAAAACAACACCTGTCA
                                                                                       GATTTTTTTTTGTTGAGCACAGAGGTCAGTTAAAGGTC------CAGTTG 899
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Indels:
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Percent Similarity:
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Query Match:
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US-08-957-742-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ATTOID TURK
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 716-1180 INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Shuich
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1660 bases
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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80 SerSerSerGlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCys 99
                                                                         60 SerSerValProAspGlyLysProLeuValArgGluProCysArgSerCysAlaValVal
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1941 Roland Clarke Place
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(703) 71
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VENTION: Sia' 2,3Gala 1,4G1cNAc '
VENTION: SIALYLTRANSFERASE
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Search completed: December 21, 2004, 22:52:56
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1071 ---GATCTGCCCTACCACTACTATGACAAA 1097
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO spool/US100.99114/runat 21122004 100142 3479/app query.fasta_1.455
-Q=/cgn2 1/USPTO spool/US100.99114/runat 21122004 100142 3479/app query.fasta_1.455
-DB=Publlished Applications NA -QFMT=fastap -SUFFTX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10019114 @CGN 1 1 480 @CRN nat 21122004 100142 3479
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Ygapop 10.0, X
Fgapop 6.0, I
Delop 6.0, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*

1. /ggn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2. /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3. /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4. /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5. /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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jn2 6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
jn2 6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
jn2 6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
jn2 6/ptodata/1/pubpna/US10E_PUB.seq:*
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G/ptodata/1/pubpna/US08_PUBCOMB.seq:*
G/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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US-09-978-360A-2

Sequence 2, Application US/09978360A

Publication No. US20040110939A1

GENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste Dumas Milne

APPLICANT: Bouqueleret, Lydie

APPLICANT: Bouqueleret, Lydie

APPLICANT: Jobert, Severin

CURRENT TILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: US 60/069,957

PRIOR APPLICATION NUMBER: US 60/069,957

PRIOR APPLICATION NUMBER: US 60/074,121

PRIOR APPLICATION NUMBER: US 60/074,121

PRIOR APPLICATION NUMBER: US 60/081,563
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Percent Similarity:
Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1998-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
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ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 261..1166
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LENGTH: 1556
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LOCATION: 261..314
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.80
OTHER INFORMATION: seg RLVLIILCSVVFS/AV
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GlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgVal 160
                                                         LeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPhe 140
                                                                                                                              PheArgMetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThr
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Mismatches:
Indels:
Gaps:
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GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Domas Milne Edwards, J.B.

APPLICANT: Dobert, S.

APPLICANT: Dobert, S.

TITLE OF INVENTION: Complementary DNA's Encoding Pro
TITLE OF INVENTION: Peptides

FILE REFERENCE: GENSET.050CP3

CURRENT APPLICATION NUMBER: US/10/315,664

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: US/9/599,360

PRIOR APPLICATION NUMBER: 00/113,686

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: 60/113,686

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: 60/141,032

PRIOR APPLICATION NUMBER: 09/469,099

PRIOR FILING DATE: 1999-12-21

PRIOR FILING DATE: 1999-12-21
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US-10-315-664-25
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SOFTWARE: Patent.pm
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/10315664 Publication No. US20030203377A1
                                   FEATURE:
NAME/KEY: sig_peptide
LOCATION: 261..314
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.80
OTHER INFORMATION: seq RLVLIILCSVVFS/AV
                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 261..1166
NAME/KEY: polyA_site
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; LOCATION: 1524..1556 US-10-315-664-25

Query DB:

Percent Similarity:
Best Local Similarity:
Query Match:

1.17e-196 1626.00 100.00% 100.00% 100.00% 100.00%

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US-10-019-114A-7 (1-302) x US-10-315-664-25 (1-1556)
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                                                                                                                                                                              GluLysSerHisProSerValProTyrHisTyrPheGluLysGlyArgLeuAspGluCys
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                   GCGGTCTTCTCCCGCTGGGCCAAGAAGAGGCCCATCGTGTTCGCCCATCCGTCCTGGAGG
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CURRENT APPLICATION NUMBER: US/09/895,298
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
LENGTH: 1735
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; NAME/KEY: SITE
; LOCATION: (1002)
; OTHER INFORMATION: n
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US-09-895-298-15
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Publication No. US20030078405A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 47 Human Secreted Proteins
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ORGANISM: Homo sapiens
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GlnLysAlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgVal 160
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                                                 LeuArgValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPhe 140
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APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValTyrThrPheThrGluArgMetMetAlaTyrCysAspGlnIlePheGlnAspGluThr
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                                                                                     Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
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o. US20040038223A1
                                                         ENCODING
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SEQ ID NO 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (421)..(1074)
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PRIOR FILING DATE: 2001-10-02
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LOCATION: (5)..(5)
OTHER INFORMATION: Wherein n
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NAME/KEY: misc_feature
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OTHER INFORMATION: Wherein n may be
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OR APPLICATION NUMBER: 60/373,815
OR FILING DATE: 2002-04-19
OR APPLICATION NUMBER: 60/327,917
OR FILING DATE: 2001-10-09
OR APPLICATION NUMBER: 60/381,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR FILING DATE: 2002-05-16

RAPPLICATION NUMBER: 60/328,056

DR FILING DATE: 2001-10-09

DR APPLICATION NUMBER: 60/373,260

DR FILING DATE: 2002-04-17

DR FILING DATE: 2002-04-19

PR FILING DATE: 2002-04-19
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APPLICATION NUMBER: 60/328,029
FILING DATE: 2002-10-09
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                          GlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThrLeuArgValVal
                                                                            ATGCTGGGCTCAGGCCTGGGTGCTGAGATCGACAGTGCCGAGTGCGTGTTCCGCATGAAC
                                                                                                MetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCysValPheArgMetAsn
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RESULT 4 US-10-262-511-183

Sequence 183, Application No. US20 GENERAL INFORMATION:

APPLICANT: Smithson, Glennda APPLICANT: Millet, Isabelle APPLICANT: Peyman, John A. APPLICANT: Kekuda, Ramesh

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Jingtang

Xiaojia (Sasha)

APPLICANT: APPLICANT: APPLICANT:

Ellerman, Karen Malyankar, Uriel M. Patturajan, Meera Spytek, Kimberly A. Edinger, Shlomit R.

Tatiana

APPLICANT:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Miller, Charles E Ji, Weizhen Catterton, Elina

APPLICANT: APPLICANT:

> Zerhusen, Bryan D. Anderson, David W. Gorman, Linda

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ACTGAG 1198 ThrGlu

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APPLICANT: Howes, Steven H.

APPLICANT: Resnick, Richard J.

APPLICANT: Gulukota, Kamalakar

APPLICANT: Gulukota, Kamalakar

APPLICANT: Graham, James R.

APPLICANT: Graham, James R.

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6401

CURRENT APPLICATION NUMBER: US/09/823,245A

CURRENT FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/194,941

PRIOR APPLICATION NUMBER: 60/194,941

PRIOR FILING DATE: 2000-04-06

NUMBER OF SEQ ID NOS: 631

SOCTMARE: Patentin Ver. 2.0

LENGTH: 743
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Publication No. US20020039760A1
GENERAL INFORMATION:
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-823-245A-30
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ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/09/895,298
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1998-12-18
PRIOR PPLICATION NUMBER: 60/113,006
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR PILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PATENTIN OF SEQ ID NOS: 231
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 121
LENGTH: 966
TYPE: DNA
ORGANISM: Homo sapiens
 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: 47 Human Secreted Proteins FILE REFERENCE: PZ035P1
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                                                                                                                                Query Match:
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; NAME/KEY: misc_feature
; OTHER INFORMATION: rat
US-10-844-874-19
                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                               SEQ ID NO 19
LENGTH: 2956
TYPE: DNA
ORGANISM: Rat
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Moskal, Joseph
APPLICANT: Yamamoto, Hirotaka
TITLE OF INVENTION: Detection and Treatment
FILE REFERENCE: 97-186-E
FURRENT APPLICATION NUMBER: US/10/844,874
CURRENT FILLING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 20
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                                                CTTTCCCTTTGCTCCTGAACTGCTTTGGACAACCTAAAACCAAATGGATCCCTTTGTCCT
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No. US20040204381A1
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PRIOR FILING DATE: 2001-07-05
PRIOR PELICATION NUMBER: 60/360814
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/303828
PRIOR TILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR APPLICATION NUMBER: 60/323380
PRIOR PILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/304016
PRIOR APPLICATION NUMBER: 60/304016
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/10188186
Publication No. US20040029789A1
GENERAL INFORMATION:
APPLICANT: Anderson et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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CURRENT FILING DATE: 2002-07-02
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APPLICATION NUMBER: 60/304502 FILING DATE: 2001-07-11 APPLICATION NUMBER: 60/305262
                                                                           FILING DATE:
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/305673
PRIOR FILING DATE: 2001-07-16
Remaining Prior Application data removed - 1
NUMBER OF SEQ ID NOS: 368
SOFTWARE: CUSTOM
SEQ ID NO 21
LENGTH: 966
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LOCATION: (19)..(934)
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alValTyrGlyMetValSerAspSerTyrCysArgGluLysSerHisProSerValProT
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                                                                                                                           etAlaTyrCysAspGlnIlePheGlnAspGluThrGlyLysAsnArgArgGlnSerGlyS
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                                                              erPheLeuSerThrGlyTrpPheThrMetIleLeuAlaLeuGluLeuCysGluGluIleV
                                                                                                           TGAGTTACTGTGATGGAGTTTTTAAGAAGGAAACTGGGAAGGACAGAGTCCAGTCTGGCT
                                                                                                                                                                    TGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGAAGCGCA
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APPLICANT: STEELIMAND, KAITHEEN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
INUMBER OF SEQ ID NOS: 14064
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11536
LENGTH: 3283
LENGTH: 3283
CORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher
APPLICANT: Steinmann, Ka
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NAME/KEY: misc_feature
LOCATION: 1, 3283
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NUMBER OF SEQ ID NOS: 4096; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 380; LENGTH: 3207; TYPE: DNA; ORGANISM: Homo sapiens US-10-104-047-380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 380, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 fu
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
PRIOR FILING DATE:
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Best Local Similarity:
Query Match:
                                                                                        US-10-019-114A-7 (1-302) x US-10-104-047-380 (1-3207)
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  FILE REFERENCE: 21402-397C
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT APPLICATION NUMBER: US/10/188,186
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: 60/30346
PRIOR FILING DATE: 2001-07-05
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
PRIOR APPLICATION NUMBER: 60/303828
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Publication No. US20040029789A1
GENERAL INFORMATION:
APPLICANT: Anderson et al.
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; LOCATION: (19)..(973)
US-10-188-186-23
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PRIOR APPLICATION NUMBER: 60/361133
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PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-19
PRIOR PRIOR APPLICATION NUMBER: 60/304502
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PRIOR PRICING DATE: 2002-04-19
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NUMBER OF SEQ ID NOS: 368
SOFTWARE: Custom
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                                                                                  euLeuGlnLeuThrArgMetTyrProGlyLeuGlnValTyrThrPheThrGluArgMetM 189
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PRIOR APPLICATION NUMBER: 60/303828
PRIOR TRILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/323380
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/361133
PRIOR FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/101 Publication No. US20040029789A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                 SOFTWARE: Custom SEQ ID NO 19
                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 368
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC FILE REFERENCE: 21402-397C
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/305262
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/373881
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PRIOR APPLICATION NUMBER: 60/304502
PRIOR FILING DATE: 2001-07-11
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PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/360814
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CURRENT FILING DATE: 2002-07-02
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                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo
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APPLICATION NUMBER: 60/305673
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Sequence 188, Application US/10097340 publication No. US20030087250A1 GENERAL INFORMATION: APPLICANT: John MONAHAN APPLICANT: Manjula GANNAVARAPU
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT APPLICATION NUMBER: 60/2-6,025
PRIOR APPLICATION NUMBER: 60/3-6,025
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/2-6,026
PRIOR APPLICATION NUMBER: 60/2-6,026
PRIOR PILING DATE: 2001-09-16
PRIOR APPLICATION NUMBER: 60/314,967
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,580
PRIOR APPLICATION NUMBER: 60/323,580
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Best Local Similarity:
Query Match:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 188
LENGTH: 2048
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Robert C. BAST,
Karen LU
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AlaArgAspThrLeuTyrMetValTrpGlyGlnGlyArgHisMetAspArgValLeuGly 162
                                                                                                                                                                                                          GlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCysValPheArg
                                                                            GTCATCGCGCATTCCAGCATCCAGAGGATCCTCCGCAACCGCCATGACCTGCTCAACGTG
                                                                                                                   ValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPheGlnLys
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Karen GLATT
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Shubhangi KAMATKAR
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Rachel E. MEYERS
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APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

FILE REFERENCE: 084335/0160

CURRENT APPLICATION NUMBER: US/10/094,749

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 00/350,435

PRIOR FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SOPTWARE: PATENTIN VET: 2.1

SEQ ID NO 802

LENGTH: 2000

TYPE: DNA

ORGANISM: Homo Sapiens
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US-10-094-749-802
                         US-10-094-749-802
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APPLICANT: SUGIYAN
APPLICANT: OTSUKI
APPLICANT: WAKAWAT
APPLICANT: SATO, F
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAMA, TSUTOMU
OTSUKA, MOTOYUKI
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SUGIYAMA, 10...
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YAMAMOTO, JUN-ICHI
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Sequence 31, Application US/10286
Publication No. US20030143686A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti G.
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TACCTCTCCCATGAGCGAGGGACGCAAGGGCAGTCATCACCGCTTTATCACAGAGAAAACGA
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APPLICANT:

BURFORD,

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SEQ ID NO 31
LENGTH: 2075
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: DING, Li
TITLE OF INVENTION: TRANSFERASES
FILE REFERENCE: PI-0241 USA
CURRENT APPLICATION NUMBER: US/10/288,252
CURRENT FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: US 60/252,819
PRIOR APPLICATION NUMBER: US 60/249,639
PRIOR PPLIOR DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/249,639
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR APPLICATION NUMBER: US 60/247,931
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/244,025
PRIOR APPLICATION NUMBER: US 60/238,481
PRIOR APPLICATION NUMBER: US 60/238,481
PRIOR APPLICATION NUMBER: US 60/236,523
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030143686A1 2778782CB1
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WARREN, Bridget A.
YAO, Monique G.
TRIBOULEY, Catherine N
                                                                                           MetAsnGlnAlaProThrValGlyPheGluAlaAspValGlyGlnArgSerThrLeuArg 122
                                                                                                                                                                        GlyGlnMetLeuGlySerGlyLeuGlyAlaGluIleAspSerAlaGluCysValPheArg 102
ValValSerHisThrSerValProLeuLeuLeuArgAsnTyrSerHisTyrPheGlnLys 142
                                                             ATGAATGACGCCCCACACGCGGCTATGGGCGTGACGTGGGCAATCGCACCAGCCTGAGG
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GRIFFIN, Jennifer A.
SANJANWALA, Madhu S.
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LEE, Ernestine A.
HAFALIA, April J.A.
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1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyArgThrTyrArgThrLeuLeuGlnLeuThrArgMetTyrProGlyLeuGlnValTyr 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCAGGGCACCGTGTTCATCTTCTGGGGCCCCAGCAGCTACATGCGGGGGGACGGCAAG
                                                                                         ValPheSerArgTrpAlaLysLysArgProIleValPheAlaHisProSerTrpArgThr 301
                                                                                                                                                                                                                   SerHisProSerValProTyrHisTyrPheGluLysGlyArgLeuAspGluCysGlnMet
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                                                            GTCTTTAAGAACTGGGCACGGACATTCAATATTCACTTTTTTCAACCAGACTGGAAACCA 1187
                                                                                                                                                        TyrLeuAlaHisGluGlnAlaProArg---SerAlaHisArgPheIleThrGluLysAla
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Search completed: December 22, Job time : 610 secs 2004, 00:16:15

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Result
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is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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        GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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                              US-09-599-360B-75
US-09-334-601-13
US-09-621-976-3915
US-08-446-875-16
US-08-503-133A-2
US-08-503-133A-2
US-08-503-133A-2
US-08-503-133A-2
US-08-972-498-2
US-08-99-545-2
US-08-08-626-994A-3
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US-08-666-3678-6
US-08-957-742-1
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1 US-08-446-777-6 1 US-08-446-777-8 1 US-09-34-601-22 2 US-09-334-601-24 4 US-10-102-002-462 4 US-08-361-3048-2 2 US-08-310-385G-18 3 US-09-334-601-25 3 US-09-334-601-26 1 US-07-991-5878-7 1 US-08-102-385G-12 2 US-08-102-385G-12 2 US-08-102-385G-12 2 US-08-102-385G-12 2 US-08-102-385G-12 2 US-08-102-385G-12	55	77	384	332	332	329	329	90	90	90	340	356	600	90	90	767	767	
US-08-446-777-6 US-08-446-777-8 US-09-334-601-22 US-09-334-601-22 US-08-361-304A-2 US-08-102-385G-18 US-09-334-601-25 US-09-334-601-25 US-09-334-601-25 US-09-334-601-26 US-07-991-587A-7 US-08-406-875-12 US-08-406-875-12 US-08-102-385G-12 US-08-102-385G-12 US-08-102-385G-12 US-08-102-385G-15	N	N	w	N	N	_	_	w	ω	w	2	4.	4.	w	ω	_	1	
	US-08-102-385G-15	US-08-102-385G-29	US-09-334-601-8	US-08-102-385G-12	US-08-446-875-12	US-08-309-985-7	US-07-991-587A-7	US-09-334-601-26	US-09-334-601-25	US-09-334-601-23	US-08-102-385G-18	US-08-361-304A-2	US-10-140-002-462	US-09-334-601-24	US-09-334-601-22	US-08-446-777-8	US-08-446-777-6	
	15,	29,	8, 2	12,	12,	7, 1	7, 1	26,		•	18,	2, 1	462	24,	22,	8, 2	6, 2	
66, 1 88, 1 224, 224, 2462, 1 118, 1 118, 1 112, 1 112, 1 112, 1	App	App	App1	App	App	Appl	pp1	Appl	Appl	Ąpp	App	App1	· Ap	Ąpp	App	Appl	pp1	

ALIGNMENTS

RESULT 1 US-09-599-360B-75

Sequence 75, Application US/09599360B Patent No. 6548633
GENERAL INFORMATION:

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SOFTWARE: Patent.pm
SEQ ID NO 75
LENGTH: 302
TYPE: PRT
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APPLICANT: Bougueleret, L.
APPLICANT: Jobert, S.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides, FILE REFERENCE: GENSET. 050CP3
CURRENT FAPLLCATION NUMBER: US/09/599.360B...

CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: SIGNAL
LOCATION: -18..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 302; Conserv
                                       181
241 EKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHRFITEKAVFSRWAKKRPIVFAHPSWR 300
                                                                             181
                                                                                                                       121 LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                               121 LRVVSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQ
                                                                                                                                                                                                   61 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRST
                                                                                                                                                                                                                               61 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMAQAPTVGFEADVGQRST
                                                                                                                                                                                                                                                                                 1 MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
                                                                                                                                                                                                                                                                                                            1 MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
                                                               VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                       VYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCR
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1626; DB 4; 100.0%; Pred. No. 3.4e-170; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 302;
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APPLICANT: Kapitonov, Dmitri
APPLICANT: Yu, Robert
ITTLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT FILING DATE: 199-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
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US-09-334-601-13
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-334-601-13
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3915
                                                                                                                                                                                                                                                                                                                                                                 Sequence 3915, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.3*; Score 639.5; DB 3; Length 336; Best Local Similarity 47.9*; Pred. No. 1.1e-61; Matches 125; Conservative 44; Mismatches 89; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09334601 Patent No. 6280989
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                     TITLE OF INVENTION: ESTs and Encoded Human Proteins. FILE REFERENCE: GENSET.054PR2
                                                       ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -18..-1
                                                                                        LENGTH: 95
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 GRTYRTLLQLTRMYPGLQVYTFTERNMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILAL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 MNDAPTRGYGRDVGNRTSLRVIAHSSIQRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 TQQRPGVPAGPRPLDGYLGVADHKPL-KMHCRDCALVTSSGHLLHSRQGSQIDQTECVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 TGSRPTVP-GPLHFSGYSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFKNWARTFNIHFFQPDWKPE 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELCEBIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPR-SAHRFITEKA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQVYNNLHLLSQVLPRLKAFMITRHKMLQFDELFKQETGKDRKISNTWLSTGWFTMTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-446-875-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                APPLICATION NUMBER: US/08/446,875
PILING DATE: JULY 12, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/102,385
PILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                 TELEFAX: (310) 277-129
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 56
OTHER INFORMATION:
NAME/KEY: UNSURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burlingame, Alma L.
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
NUMBER OF SEQUENCES: 16
CORRESO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNSURE LOCATION: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
MOLECULE TYPE: protein
-446-875-16
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 90067
                                                 TYPE: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEID 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKAPGRLVLIILCSVVFSAVYILLCCWAGLPLCLATCLDHHFPTGSRPTVPGPLHFSGYS
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USA
                                            amino acid
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                                                                                                               ង៖ (310)
(310) 27
                                                               340 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paulson, James C
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                                                                                                                  277-1297
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                                                                                                                                  788-5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brian Duane
                                                                                                   16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 494; DB 4;
Pred. No. 1.7e-46;
                                                                                                                                                                                                                                                                                                                                                            #1.25
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US-08-503-133A-2
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                                                                     Matches
                                                                                      Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Gerardy-Schahn, Rita; Fukuda, Minoru;

APPLICANT: Nakayama, Jun; Eckhardt, Matthias

APPLICANT: Nakayama Jun; Eckhardt, Matthias
                                                                                                                                                                                                                                                 TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
                                                                                                                                                           TOPOLOGY: 11: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/503,133A
FILING DATE: 17-JULY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/04289
FILING TERMS TO THE PRIOR PRIOR NUMBER: PCT/EP94/04289
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: EDITELECOMMUNICATION INFORMATION
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            TELEPHONE: (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                           NAME: Hanson, No. 5747326man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 DSYCREKSHPSVPYHYFE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 YPGLQVYTFTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 LRNYSHYFQKARDTLYMVWGQGRHMD-----RVLGGRTYRTLL------QLTRM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 CRRCAVVGNSGNLRESSYGPEIDSHDFVLRMNKAPTAGFEADVGTKTTHHLV-----
                               59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.
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                                                                                    Similarity
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DS--KGNWH-----HYWE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                               359 amino acids
                                                                 12.1%; Score 196.5; DB 1 ilarity 27.5%; Pred. No. 6.4e-13; Conservative 39; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette,
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Isolated Polysialyl Transferases,
Nucleic Acid Molecules Coding Therefor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS
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                                                                                                                                                                                                                                                                                                                          BOER 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 198.5; DB 2;
Pred. No. 3.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GRYPSTGILSVIFSMHVCDEVDLYGFGA 291
                                                                                                   DB 1;
                                                                     98;
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                                                                     Indels
                                                                                                    Length 359;
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                                                                 Gaps
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                                                                                                                                                     US-08-576-775A-2
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                                                                           Matches
                                                                                                               Query Match
                                                                                                                                                                                                                                                                   TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gerard
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/50: FILING DATE: 17-July-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-December-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
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TITLE OF INVENTION:
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                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5849904max REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/576,775A FILING DATE: 21-December-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York City
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 SDFITMNPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL 243
125 HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKBIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 LNVLHNRGALK 350
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                                   59 YSSVPDGKPLVREPCRSCAVYSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                               359 amino acids
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NYENTION: Isolated Polysialyl Transferases,
NYENTION: Nucleic Acid Molecules Coding Therefor, Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                           Conservative
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                                                                       12.1%; Score 196.5; DB 2
27.5%; Pred. No. 6.4e-13;
tive 39; Mismatches 98
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                                                                                                             DB 2;
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                                                                           Indels
                                                                                                             Length 359;
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                                                                         Gaps
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                                   Matches
                                                                     Query Match
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                               TELEFAX: (212) 838-38
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gerardy-Schaim, ....APPLICANT: Nakayama, Jun; Eckhardt, Matthias
APPLICANT: Nakayama, Jun; Eckhardt, Matthias
TITLE OF INVENTION: Isolated Polysialyl Transferases,
TITLE OF INVENTION: Nucleic Acid Molecules Coding Therefor, Methods of
                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                 NAME: HAHBON, NO. 5959078ma
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
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STREET: New York City
STATE: New York
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-July PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/576,775
FILING DATE: 21-December-1995
APPLICATION NUMBER: 08/503,133
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                     LENGTH:
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59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
                                 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDFITMNPSVVQRAFGGFRNESDRAKFVHRLSMLNDSVLWIPAFMVKGGEKHVEWV-NAL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL----YMVWGQGRHMDRVLGGR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     805 Third Avenue
                                                                                                                                                                                       359 amino acids
                                                                                                                                                                                                                                                   (212)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PS/2
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                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 3.5 inch, 360 kb storage
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                                                                                                                                                                                                                           2) bc;
, 838-3884
, NO: 2:
                                                                                                                                                                                                                                                                                                                                             No. 5959078man D.
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                                   12.1%; Score 196.5; DB 2; 27.5%; Pred. No. 6.4e-13; tive 39; Mismatches 98;
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                                                                       Length 359;
                                       Indels
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                                     45;
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US-08-899-545-2
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                                                                                                                                   US-08-899-545-2
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                                                                  Matches
                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gerard
APPLICANT: Nakaya
                                                                                                                                                                                                         TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTATION SYSTEM: PC-1005
OPERATING SYSTEM: PC-1005
SOFTWARE: WOrdperfect
SOFTWARE: WORDPER: US/08/899,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & L.
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 60 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                 Local Similarity
es 69; Conserv
                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                TELEPHONE:
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                              59 YSSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQR 118
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HSLLPEVSPMKNRRFKTCAVVGNSGILLDSGCGKEIDSHNFVIRCNLAPVVEFAADVGTK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLATRFCDEIHLYGFW--PFPKDLNGKAVKYHYYD----DLKYRYFSNASPHRMPLEFKT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08899545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerardy-Schahn, Rita; Fukuda, Minoru;
Nakayama, Jun; Eckhardt, Matthias
VENTION: Isolated Polysialyl Transferases.
                                                                                                                                                                                                   359 amino acids
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PS/2
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                                                                                                                                                                                                                                                                    (212)
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                                                                                  12.1%;
27.5%;
                                                                                                                                                                                                                                                                  688-9200
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                                                                  39;
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                                                                                  Score 196.5; DB 3
Pred. No. 6.4e-13;
                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 kb storage
                                                                                                   DB 3;
                                                                    98;
                                                                                                 Length 359;
                                                                    Indels
                                                                    45;
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                                                                    Gaps
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US-08-446-875-2
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US-08-446-875-2
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                                                                         Query Match 11.7%; Score 191; DB 2; Length 343; Best Local Similarity 30.0%; Pred. No. 2.4e-12; Matches 57; Conservative 36; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/102,385
FILLING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
                                                                                                                                                                                                                                                                                TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                               TYPE: amino acids
TYPE: amino acids
TOPOLOGY: line
(OLECTION)
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Poms, Smi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
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FILING DATE: July 12, 1995
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133 PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90067
                  PLVRE---PCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STLRVVSHTSVPLL---LRNYS-----HYFQKARDTL-----YMVWGQGRHMDRVLGGR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Poms, Smith, Lande & Rose
2029 Century Park East, Suite 3800
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Burlingame, Alma L.
Medzihradszky, Katalin
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Gillespie, William
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Wen, Xiaohong
Wen, Brian Duane
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US-08-102-385G-2
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                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-102-385G-2
                                                                                                                                Query Match
Best Local Similarity 30.0
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (310) 277-12
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/925369
FILING DATE: 04-AUG-1992
ATTORNEY_AGENT INFORMATION:
NAME: Oldenkamp_David_J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97-062
TELECOMMUNICATION INFORMATION:
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APPLICANT: Paulson
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/102,385G
FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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CITY: Log Angeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT 183
124 VSHTSVPLLLRNYSHYFQKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQVYT 183
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                                                           133 PLLEKRLVSCRRCAVVGNSGNLKESYYGPQIDSHDFVLKMNKAPTEGFEADVGSKTTHHF 192
                                                                                                                                                                                                                                                                                      amino acid
                                                                                       PLVRE---PCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRV 123
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                                                                                                                                                                                                                                                                                                                                                                       %: (310)788-5000
(310) 277-1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Gillespie, William
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Wen, Brian Duane
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                                                                                                                                           11.7%; Score 191; DB 2; 1 30.0%; Pred. No. 2.4e-12; tive 36; Mismatches 77;
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US-08-626-994A-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 716-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 774.
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 1.44 di
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Arnold Turk
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: A CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US FILING DATE: April 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 FTERMMAYCDQIFQDETGKNRRQSGSFLSTGWFTMILALELCEEIVVYGMVSDSYCREKS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 VYPESFRELAQEVS------MILVPFKTTDLEWVISATTTGTISHTYVPVPA-KIKV 242
                                 221
                                                                   212 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                                                                                                     169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
                                                                                                                                         165 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW------IPAFFFHT
                                                                                                                                                                           120 TLRVVSHTSVPLLLRNYSHYFQKARDTL-----YMVWGQGRHMDRVLGGRTYRT
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                                                                                                                                                                                                                                                 60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
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Y: U.S.A.
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                              ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                                                                                                     SLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQEIDKSDFVSRCNFAPTEAFHKDVGRKT
ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 300
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1941 Roland Clarke Place
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VENTION: Sia' 2,3Gala 1,4GlcNAc '
VENTION: SIALYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                              not relevant
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RESULT 12
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/ACENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
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ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1+ (ASCII) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 1.44 di
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SOFTWARE: Word Daver-
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STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
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                                                                                                                                   165
                                                                                                                                                             120 TLRVVSHTSVPLLLRNYSHYFQKARDTL------YMVWGQGRHMDRVLGGRTYRT
                                                                                                                                                                                               105 ŚLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQBIDKSDFVSRCNFAPTBAFHKDVGRKT 164
268
                                                                                            169 LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL
                                                                                                                                                                                                                              60 SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
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                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                               SATVTRTL----VDFFVEHRGOLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL
                             ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                 NLT----TFNPSILEKYYNNLLTIODRNNFFLSLKKLDGAILW--
ASAICEETHLYGFWPFGFDPNTRE----DLPYHYYDK 300
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IVENTION: Sia' 2,3Gala 1,4G1cNAc ' 2,8-

VENTION: SIALYLTRANSFERASE
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linear
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Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                      DB 3;
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US-08-626-994A-1 RESULT 13

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Sequence 1, Application US/08626994A Patent No. 5798244 GENERAL INFORMATION:

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                                                                                                                                     Sequence 1, Application US/08957742
PATENT NO. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia` 2,3Gala 1,4G1CNAC '
TITLE OF INVENTION: SIALYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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STREET:
STREET:
CITY: Reston
Virginia
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FILING DATE: April 3, 19
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: WS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/0
PILING DATE: April 3, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 11.7%; Score 190.5; DB 1; Local Similarity 30.0%; Pred. No. 3e-12; hes 65; Conservative 28; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: no
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STATE: Virginia
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                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 NLT----TENPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGABIDSAECVFRMNQAPTVGFBADVGQRS 119
                                                              E: Greenblum & Bernstein, P.L.C
1941 Roland Clarke Place
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1941 Roland Clarke Place
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VENTION: Sia' 2,3Gala 1,4G1cNAc '
VENTION: SIALYLTRANSFERASE
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JF 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold Turk
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                      APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
TITLE OF INVENTION: PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 716-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
  OPERATING SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 30.0 nes 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compactate
OPERATING SYSTEM: MS-DOS
SOPTWARE: Word Perfect 5.1+ (ASCII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                       CITY: Washington
                                         COMPUTER:
                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 SLLPDVSPIMNKRYNVCAVVGNSGILTGSQCGQBIDKSDFVSRCNFAPTEAFHKDVGRKT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 ASAICEEIHLYGFWPFGFDPNTRE----DLPYHYYDK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 SATVTRTL----VDFFVEHRGQLKVQLAWPGNIMQHVNRYWKNKHLSPKRLSTGILMYTL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 NLT----TFNPSILEKYYNNLLTIQDRNNFFLSLKKLDGAILW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 TLRVVSHTSVPLLLRNYSHYFQKARDTL-----YMVWGQGRHMDRVLGGRTYRT 168
                                                                                                20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLQLTRMYPGLQVYTFTER-----MMAYCDQIFQ--DETGKNRRQSGSFLSTGWFTMIL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSVPDGKPLVREPCRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALELCEEIVVYGMVS---DSYCREKSHPSVPYHYFEK 254
                                                                                                                                         D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 amino acids
                    SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                    U.S.A.
SYSTEM: MS-DOS
Wordperfect 5.1
                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: 1.44 diskette
IBM PC compatible
                                                           Diskette, 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 190.5; DB 3; 30.0%; Pred. No. 3e-12; tive 28; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/957,742
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                                                             1.44
                                                               쿬
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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Search completed: December 10, 2004, 18:26:42 Job time : 40 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.9%; Score 178; DB 2; Length 355; Best Local Similarity 25.2%; Pred. No. 6.8e-11; Matches 63; Conservative 37; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,367B
FILING DATE: AUGUST 19, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                       333 FNLEKQVWKR 342
                                                                                                                                                                                                                                                            231 FLNYYGRRPRERFDEDFTMNKYLVAHPDFL---RYLKNRFLKSKNLQKPYWRLYRPTTGA 287
                                                                                                                                                                                                                                                                                                    182 ------YTFTERMMAYCDQIFQDETGKNRRQSGSFL------STGW 215
                                                                                                                                                                                                                                                                                                                                               186 LONLGHKGFKKI------POGKHI-----RYIHFLEAVRDYEWLKALLLDKDIRKG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                  216 FTMILALELCEEIVVYGMVSDSYCREKSHPSVPYHYFEKGRLDECQMYLAHEQAPRSAHR 275
                                                                                                                                                                                                                                                                                                                                                                                       133 LRNYSHY-FOKARDTLYMVWGQGRHMDRVLGGRTYRTLLQLTRMYPGLQV------ 181
                                                                                                                                  276 FITEKAVFSR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 CRSCAVVSSSGQMLGSGLGAEIDSAECVFRMNQAPTVGFEADVGQRSTLRVVSHTSVPLL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70; Gaps
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